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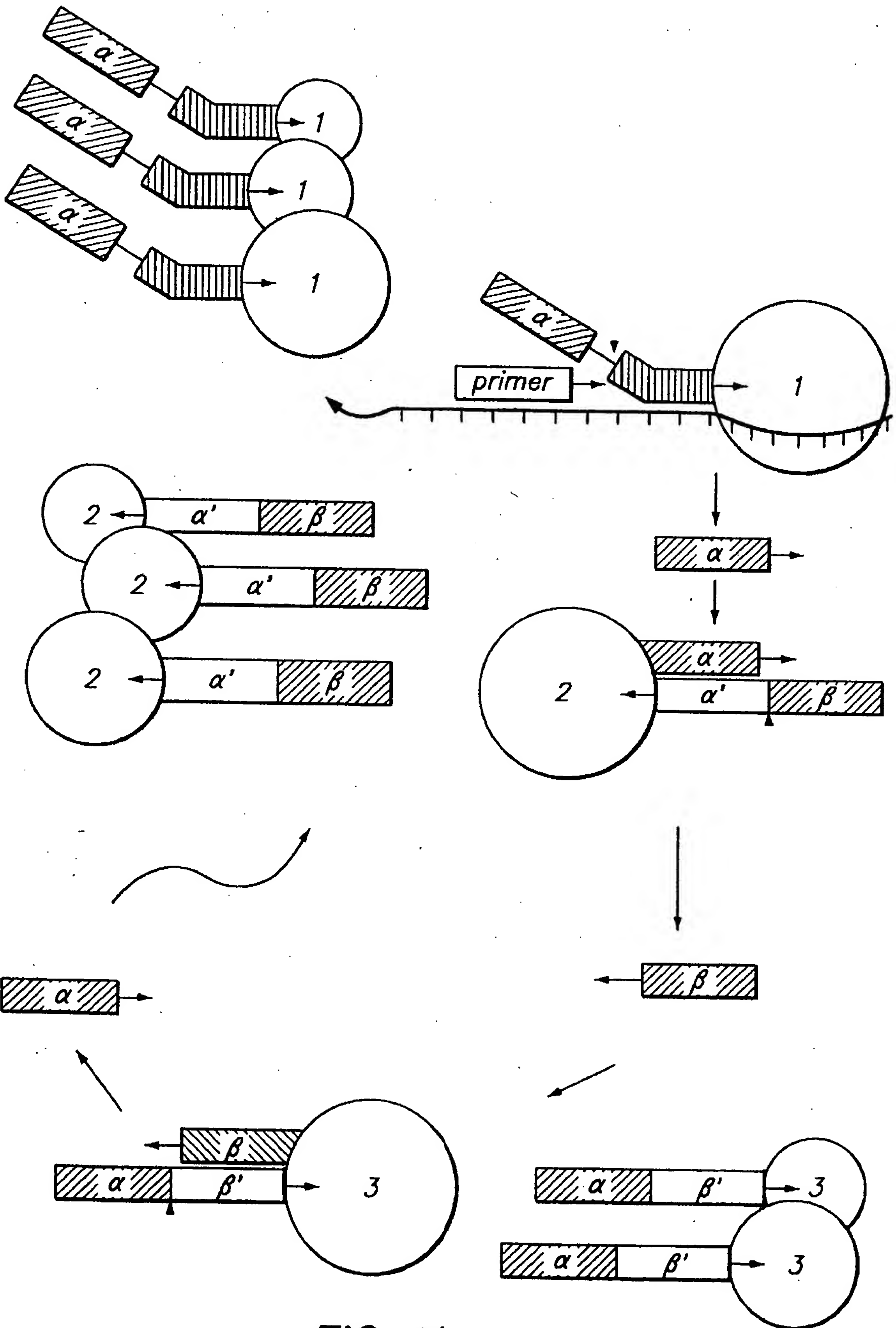


FIG. 1A

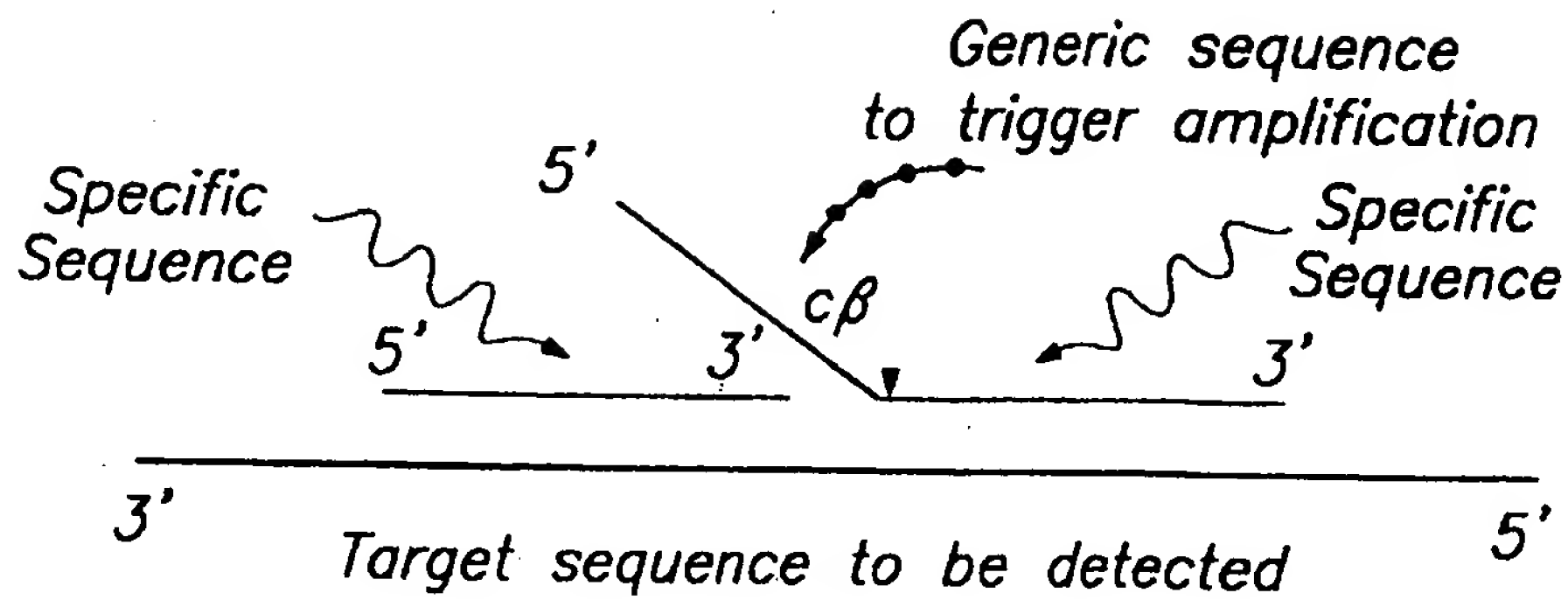


FIG. 1B PART ONE: TRIGGER REACTION

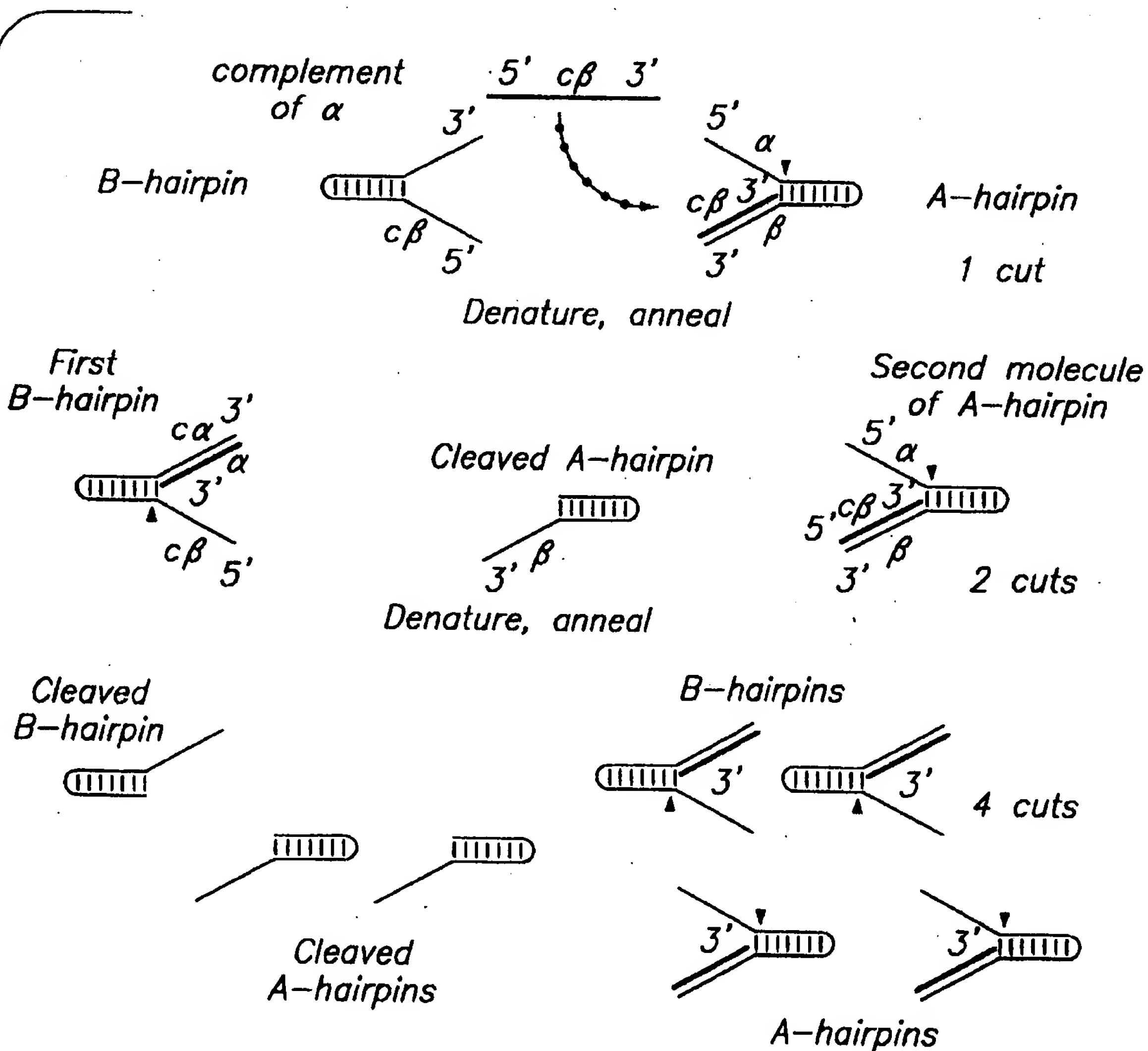


FIG. 1C PART TWO: DETECTION REACTION

[illegible]



FIG. 2B

MAJORITY [SEQ ID NO:73] CGAGCGGAGGAGGTGCTGGCCACCCTGGCCAGAGGGGGAAGAGGGGTACGAGGTGGCGCATCCTC

DNAPTAA [SEQ ID NO:13]C.....G.....C..... 417
DNAPTFL [SEQ ID NO:21] T.....G.....CG..... 414
DNAPTTH [SEQ ID NO:31]T..C..... 420

MAJORITY ACCCGGAGCGGAGCTCTACGAGCTGCTTCGGAGCGGATGGCGGTCTCCACCCGAGGGGTACCTCA

DNAPTAAAAA.....T.....CA..... 487
DNAPTFLT.....G.....G.....A.....T.....G..... 484
DNAPTTHA.....G.C.....G.....CC..... 490

MAJORITY TCACCCGCGCTGGCTTGGGAGAGTACGGCTGAGCGCGGAGGAGTGGGTGGACTACCGGGCGCTGGC

DNAPTAAC.....A.....C.....C.....CC.....A..... 557
DNAPTFLAC.....C.C.....C.....T.....C.T..... 554
DNAPTTHA.....C.....C.....T.....C.....C.T..... 560

MAJORITY GGGGAGCCCTCGGACAACTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCCGAAGCTGCTCXAG

DNAPTAA C.....GAG.....T.....G.....GAG.....T..GG.. 627
DNAPTFLG..T..A.....G.....A..G.....A..CGG 624
DNAPTTHT.....TC.....A.. 630

MAJORITY GAGTGGGGAGCCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCGGGAGAGA

DNAPTAAGC.....C.....A..... 694
DNAPTFLT..C..C.....A.....T.....T..G.....C 691
DNAPTTHA.....A.....A.AAAA.G..... 700



DNAPIAQ	DNAPIFL	DNAPIIH
.....G.....C..C..G..T..A..AA..C..G.....C..1044	T..GG..GT.....G..CC.....T.....A.....C.....G.....T.....G.....1041TG.....C.....G.....G.....GCC..G..A..A.....C.....C..1050



NAME	GRADE	INITIALS	DATE	TIME	LOCATION	REMARKS
DNAPTAQ	G.	C.	T.	AG.	T. G.	C. 1394
DNAPTFL	GG.	C.	C.	C.	C.	A. C 1391
DNAPTTH	C.	A.	T.	T.	T.	C. T. 1400



FIG. 2E

MAJORITY [SEQ ID NO:7] GGAGATCCGGCCCTCGAGGAGGAGGCTCTTGGGGCTGGCGGCGCAAGCCCTTCAAGCTCAAGTCCCGGGGAC		
DNAPTAQ [SEQ ID NO:1]	CC.....	1464
DNAPTFL [SEQ ID NO:2]	GC.....AG..G.....	1461
DNAPTTH [SEQ ID NO:3]T.....G.....	1470
MAJORITY CAGCTGGAAAGGCTGCTCTTTCAGGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAGACXGGCAAGC		
DNAPTAQ	C.....A.....	1534
DNAPTFL	GC.....G..C..G..T.....	1531
DNAPTTHTA.....T..G..G.....C..A.....A.....	1540
MAJORITY GCTCCACGAGGGCGCGTGTGTGGAGGGCCCTXCGXGAGGGCCACCCCATCGTGGAGAGATCCTGCAGTA		
DNAPTAQ	C.....C.....C.....	1604
DNAPTFL	T.....G..A.....CCGC.....	1601
DNAPTTH	G.....G.....A..G.....C.....C.....	1610
MAJORITY CGGGAGGCTCAGCAAGCTCAAGAACACCTACATXGAGCCCTGCGXGXGCTGGTCCAGCCGAGGAGGGGC		
DNAPTAQ	G.....G.....T.....G..A.....A.....	1674
DNAPTFLA.....C..C.....G.....A.....C.....	1671
DNAPTTHG..G.....C..AAG.....G.....	1680
MAJORITY CGGCTCCACAGCCGCTTCAAGCAGACGGCCACGGCCAGGGCTTAGTACCTCGGAGCCCAAGCTGC		
DNAPTAQA.....T.....G.....	1744
DNAPTFL	G.....C.....TCC.....	1741
DNAPTTHG.....	1750



FIG. 2F

MAJORITY [SEQ ID NO:7] AGAACAATCCCGCTCCGACCCGCTGGGCGAGGATCGGGCGGCGCTTGGTGGCCGAGGAGGXTGGGT

DNAPIAQ [SEQ ID NO:1]

DNAPTFL [SEQ ID NO:2]

DNAPTTH [SEQ ID NO:3]

.....G..T..G.....A.C.....G...C. 1814
.....G.....T.....C.C.....A.....C... 1811
.....CT.....C.....G...T...C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCGGGGTCTGGCCGAGCTCTCGGGGAGGAGACCTG

DNAPIAQ

DNAPTFL

DNAPTTH

A.....A.....G.....C..... 1884
.....T.T.....C.....T.....A..... 1881
.....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGAGGGGAGGACATCCACAGCCAGAGCGGCGAGCTGGATGTTGGCGTCCGCCCGG

DNAPIAQ

DNAPTFL

DNAPTTH

.....G.....GG.....G... 1954
.....T.....A.....TT...C. 1951
.....A.....A..... 1960

MAJORITY AGGCGTGGACCCCTGATCGCGCGGCGGCGCAAGACCATCAACTTCGGGGTCTCTAGCGGCAATGTCCGC

DNAPIAQ

DNAPTFL

DNAPTTH

.....A.GG..A.....T.....G... 2024
.....GG.....GG.G.....C..... 2021
..... 2030

MAJORITY CCACGCGCTCTCCAGGAGCTTGGCATCCGCTACGAGGAGCGGTGGCCCTTCATTGAGCGCTACTTCCAG

DNAPIAQ

DNAPTFL

DNAPTTH

.....A.....T.....CCA.....T... 2094
.....GG.....T..... 2091
.....TA.G.....T..A.....A 2100



FIG. 2G

MAJORITY [SEQ ID NO:7] AGCTTCCCAAGGTCCGGGCTGGATTGAGAGACCCCTGGAGGCGGAGGCGGGGCTACCTGGAGA

DNAPTAQ [SEQ ID NO:1] 2164
DNAPTFL [SEQ ID NO:2] C. CC. T. 2161
DNAPTTH [SEQ ID NO:3] A. A. G. A. C. A. 2170

MAJORITY CCCTCTTGGGCGGCGGCTACGTGCGGAGCTCAAGGCGCGGTGAAGAGCGTGGCGGAGCGGCGGGA

DNAPTAQ C. A. AG. G. C. 2234
DNAPTFL T. C. 2231
DNAPTTH AA. AA. CA. C. 2240

MAJORITY GCGCATGGCCTTCAACATGCCCGTCCAGGCGCACCGCGGAGCTCATGAAGCTGGCCATGGTGAAGCTC

DNAPTAQ T. 2304
DNAPTFL G. CG. T. 2301
DNAPTTH C. 2310

MAJORITY TTCCCGCGCTXCAGGAAATGGGGCCAGGATGCTGCTXCAGGTCCAGGAGGCTGCTCGAGGCGCC

DNAPTAQ A. GG. T. 2374
DNAPTFL T. C. G. TT. G. G. 2371
DNAPTTH G. C. G. G. C. C. G. 2380

MAJORITY CCAAGAGCGGCGGAGGXGCTGGCGGCTTGGCCAAAGGAGGTCATGGAGGGGCTCTATCCCGTGGCGGT

DNAPTAQ A. A. CC. CGG. G. 2444
DNAPTFL G. C. AG. A. GG. CAG. 2441
DNAPTTH C. C. C. A. G. AA. C. C. 2450



FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGAGGTGGGATGGGGAGGACTGGCTCTCCGCCAAGGAGTAG
DNAPTAQ [SEQ ID NO:1]A.....GA
DNAPTFL [SEQ ID NO:2]CC.....
DNAPTTH [SEQ ID NO:3]T.....GT...



FIG. 3A

MAJORITY [SEQ ID NO:8] HXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLLKALKEDG-DAYXVVVFOAK

TAQ PRO	[SEQ ID NO:4]	RG	H	I	69
TFL PRO	[SEQ ID NO:5]			V.V	68
TTH PRO	[SEQ ID NO:6]	E		YK.F	70

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEUPGYEADDVLATLAKKAEKEGYEVRIL

TAQ PRO	GG	A	S	139
TFL PRO		V	F	138
TTH PRO		FT		140

MAJORITY TADRBLYQLSDRIAVLHPGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKGI GEKTAXKLLX

TAQ PRO	K	H	D	A	T	E	R	E	209
TFL PRO		E			A	I		QR	IR 208
TTH PRO		V	V	H	F	V		L	K 210

MAJORITY EWGSLNLLKNLDRVKP-XXREKI XAHMEDLXL SXXLSXVRTDLPLEVDFAXRREPDRGLRAFLELEF

TAQ PRO	A	L	AI	L	D	K	WD	AK	K	R	278				
TFL PRO		FOH	Q	SL	LQ	G	A	A	RK	Q	H	GR	T	NL	277
TTH PRO				ENV	K	L	R	LE	R	L	QG	280			

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFULSRPEPMWAE L L A L A A A R X G R V H R A X D P L X G L R D L K E V

TAQ PRO	S	K	D	G	PE	YKA	A	348			
TFL PRO	G	A	L	SF	G	WE	L	Q	R	G	347
TTH PRO	A	AP			K	C	D	A	A	K	350



FIG. 3B

MAJORITY [SEQ ID NO:8] RGLLAKOLAVLALREGLDIXPGDDPHMLAYLLDPSNTTPEGVARRYGGWTEADAGERALLSERLFXNLXX

TAQ PRO	[SEQ ID NO:4]	S.....	G.P.....	E.....	A.....	A.....	WG	418
TFL PRO	[SEQ ID NO:5]	I.....	F.E.....	F.....	A.....	QT.	KE	417
TTH PRO	[SEQ ID NO:6]	S.....	V.....	AH.....	HR..	LK	420	

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLLEEVEFRLAGHPFNLNSRD

TAQ PRO	R...R...A.....	R.....	A.....	A.....	488
TFL PRO	K.....E.....	R.....	EA.V.O.....	487	
TTH PRO	K.....H.....	L.....	490		

MAJORITY OLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG

TAQ PRO	S.....	D.I.....	558
TFL PRO	DR.....	A.....	557
TTH PRO	R...L...Q.....	H.....	V.....	560

MAJORITY RLHTRFNOTATATGRLSSSDPNLONI PVRTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSDENL

TAQ PRO	I.....	L.....	628
TFL PRO	V..V.....	627
TTH PRO	A..A.....	630

MAJORITY IRVFQEGRDIHTQTASWNFGVPPEAVOPLMRRAKTI NFGVLYGMSAHLSDGLAI PYEEAVAFIERYFO

TAQ PRO	E.....	R.....	Q.....	698
TFL PRO	S..G.....	G..S.....	697
TTH PRO	K.....	V.....	700



FIG. 3C

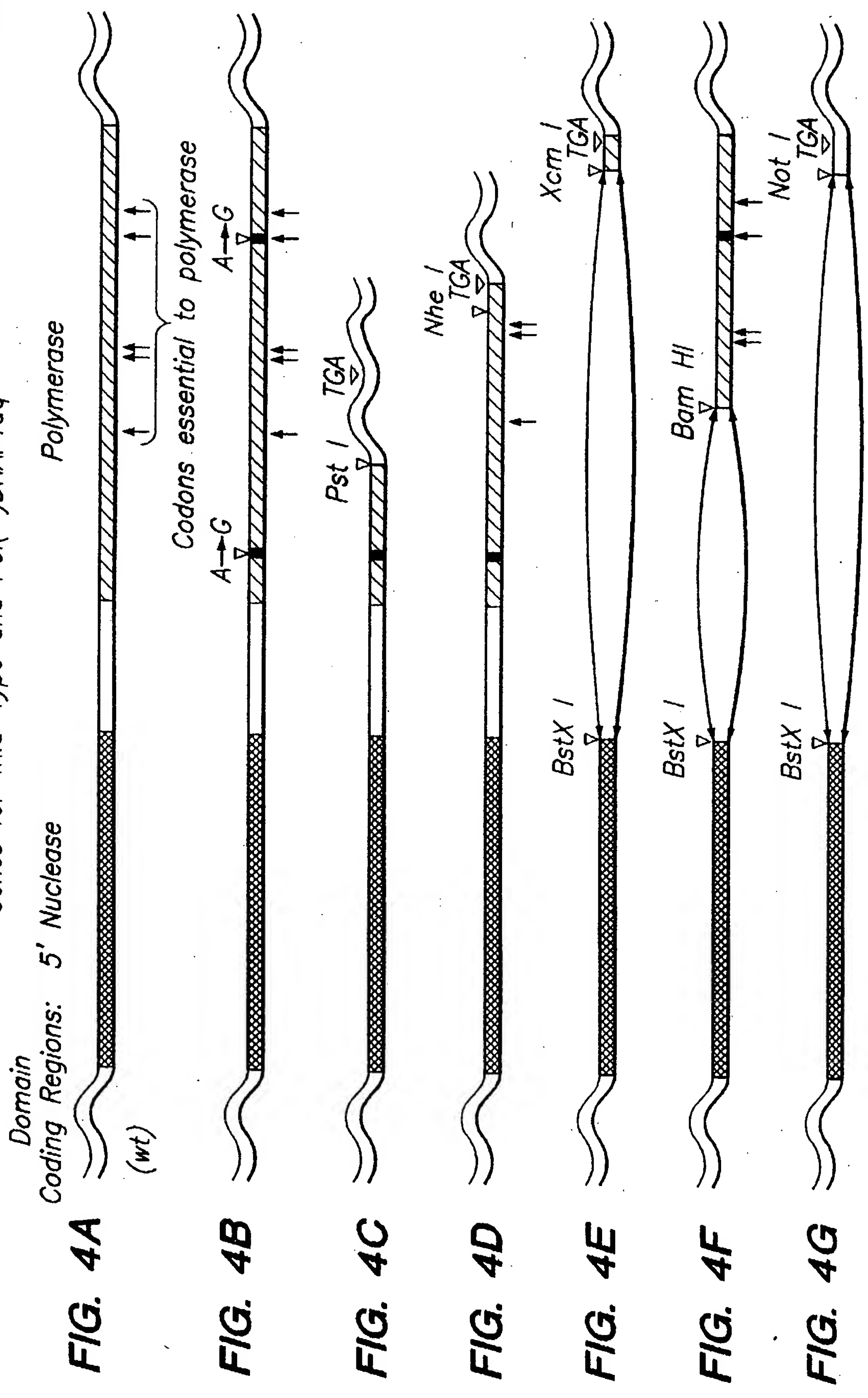
MAJORITY [SEQ ID NO:8] SFPKVRAWIEKTL EGRRGYVETLFGRRRYVPDLNARVKSVEREAAERMAFNMPVQGTADLHKLAMVKL

TAQ PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]G.....R.	767
TTH PRO	[SEQ ID NO:6]K.....	770

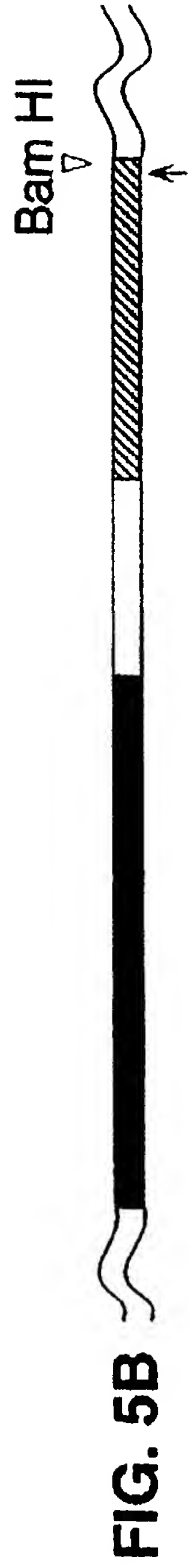
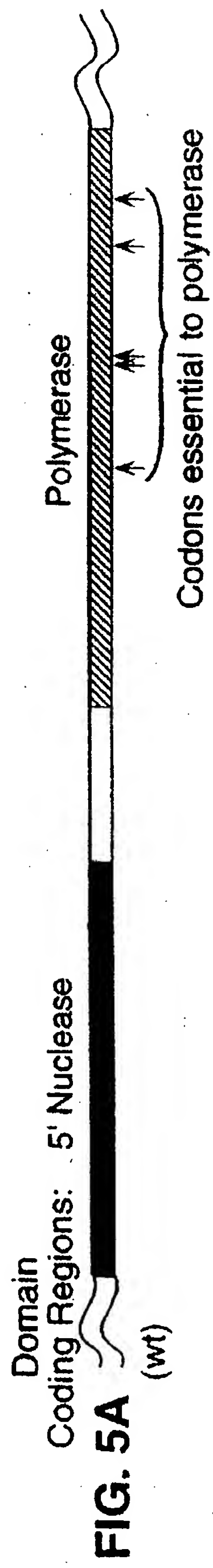
MAJORITY FPRLXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PROE.....E...A...R.....I.....	833
TFL PROQ.L.....D...R.....W..O.....L.....	831
TTH PROR.....L.....QA...E...A..KA.....M.....G	835

Genes for Wild-Type and Pol(-)DNAPTaq



Genes for Wild-Type and Pol(-) DNAPTfl



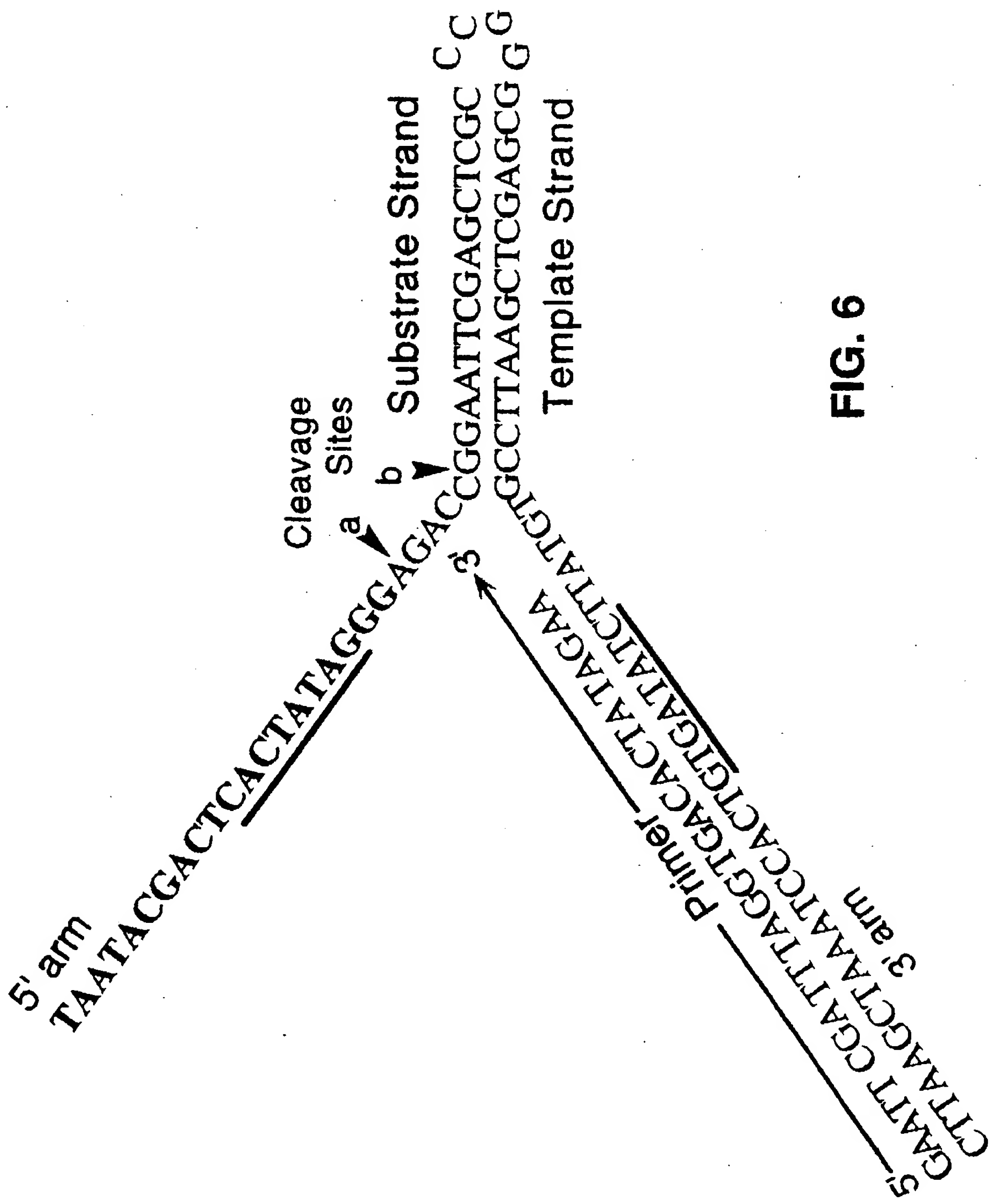


FIG. 6

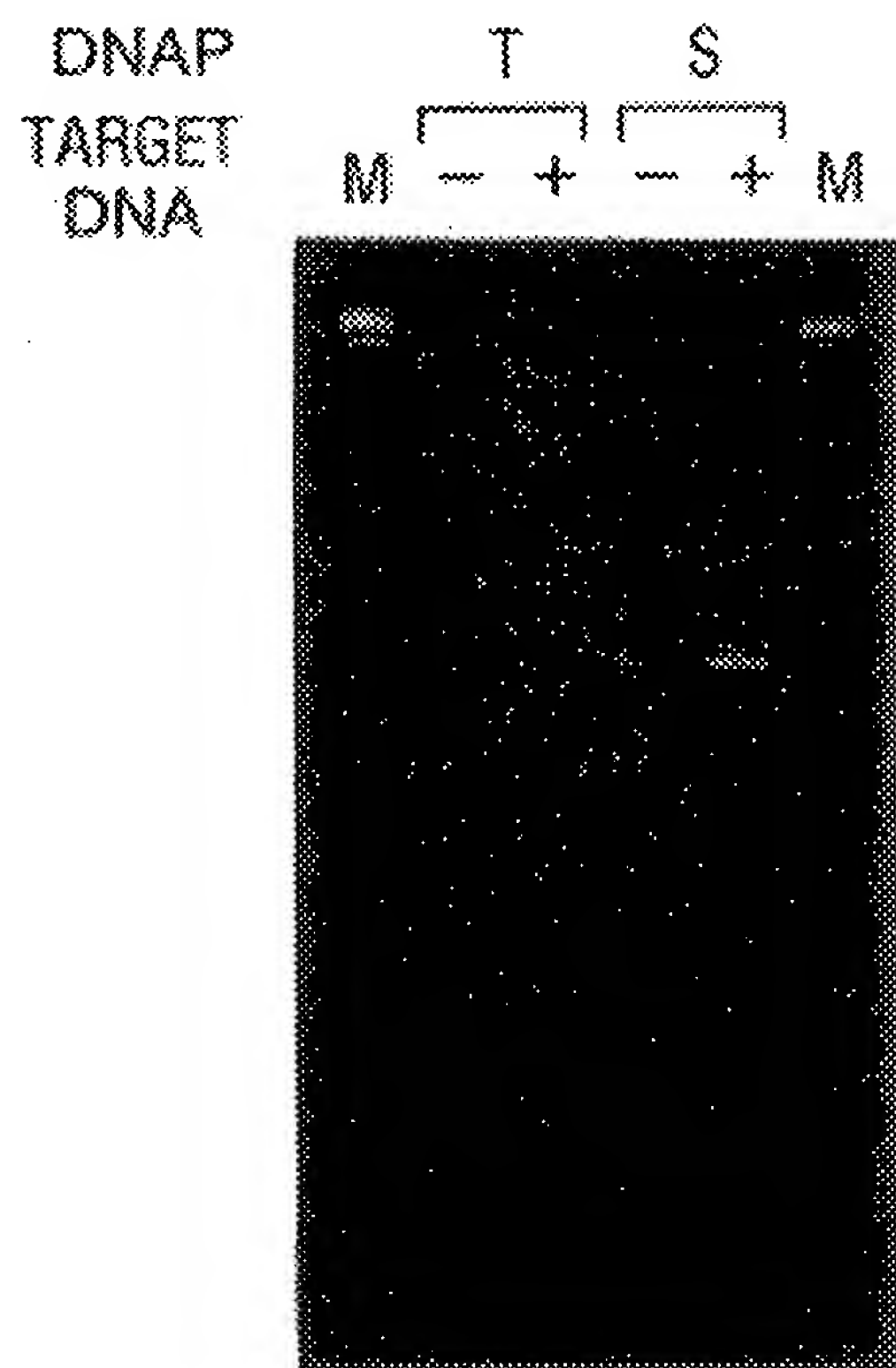


FIG. 7

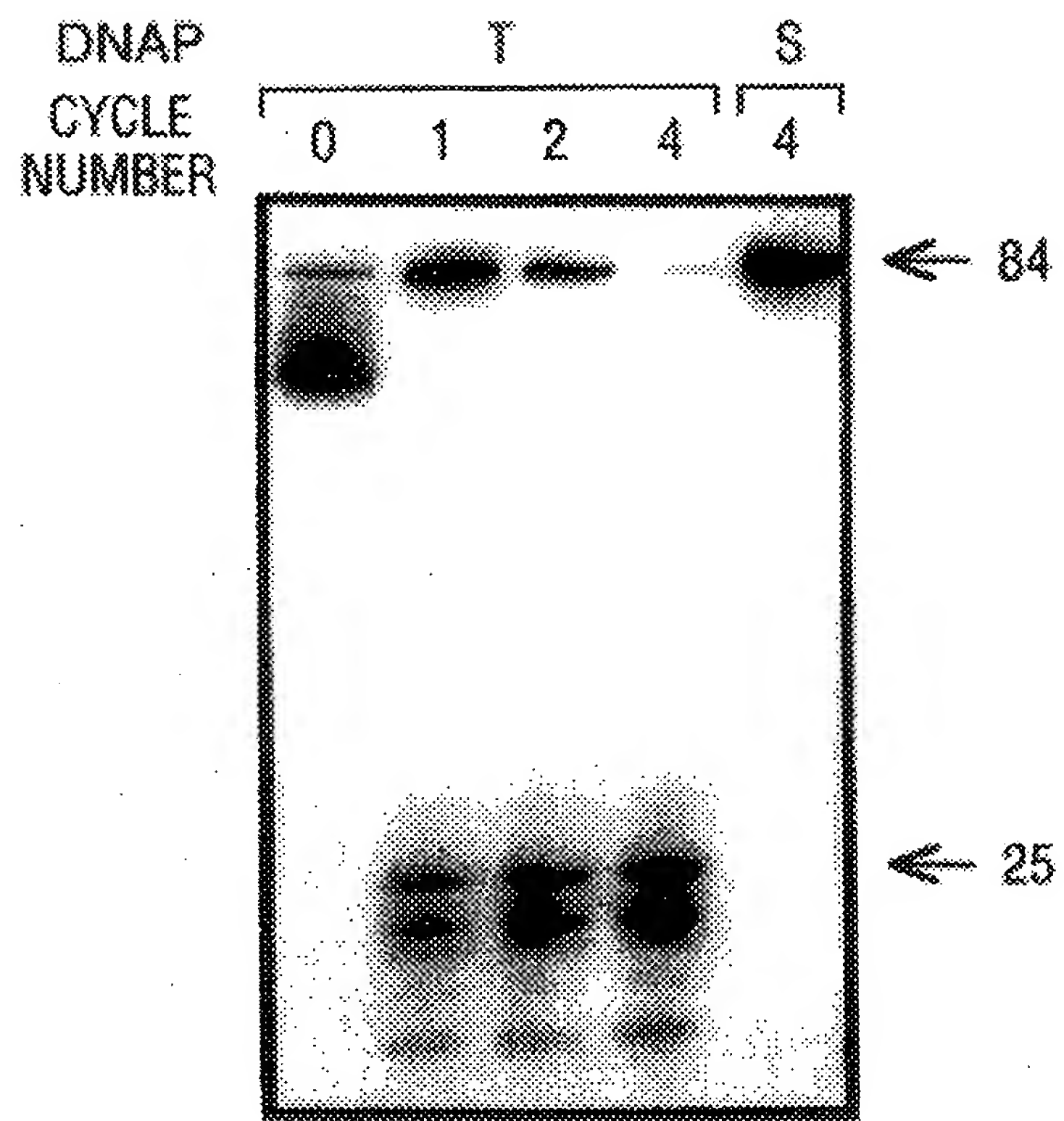


FIG. 8



	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

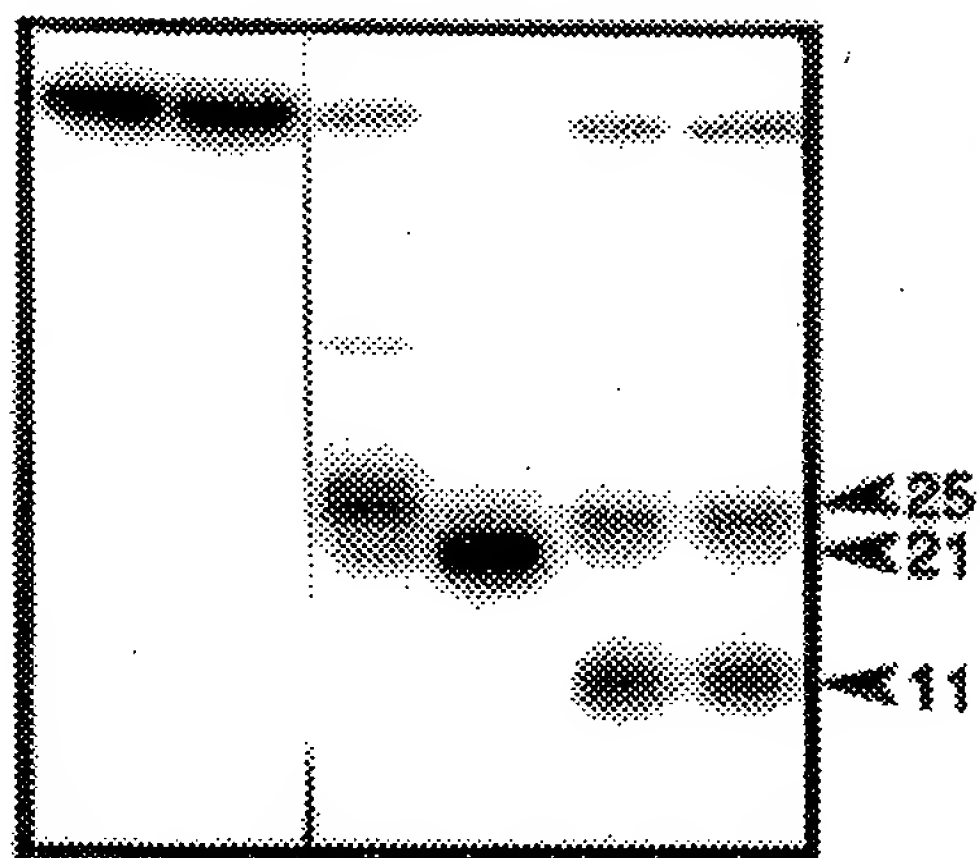


FIG. 9A

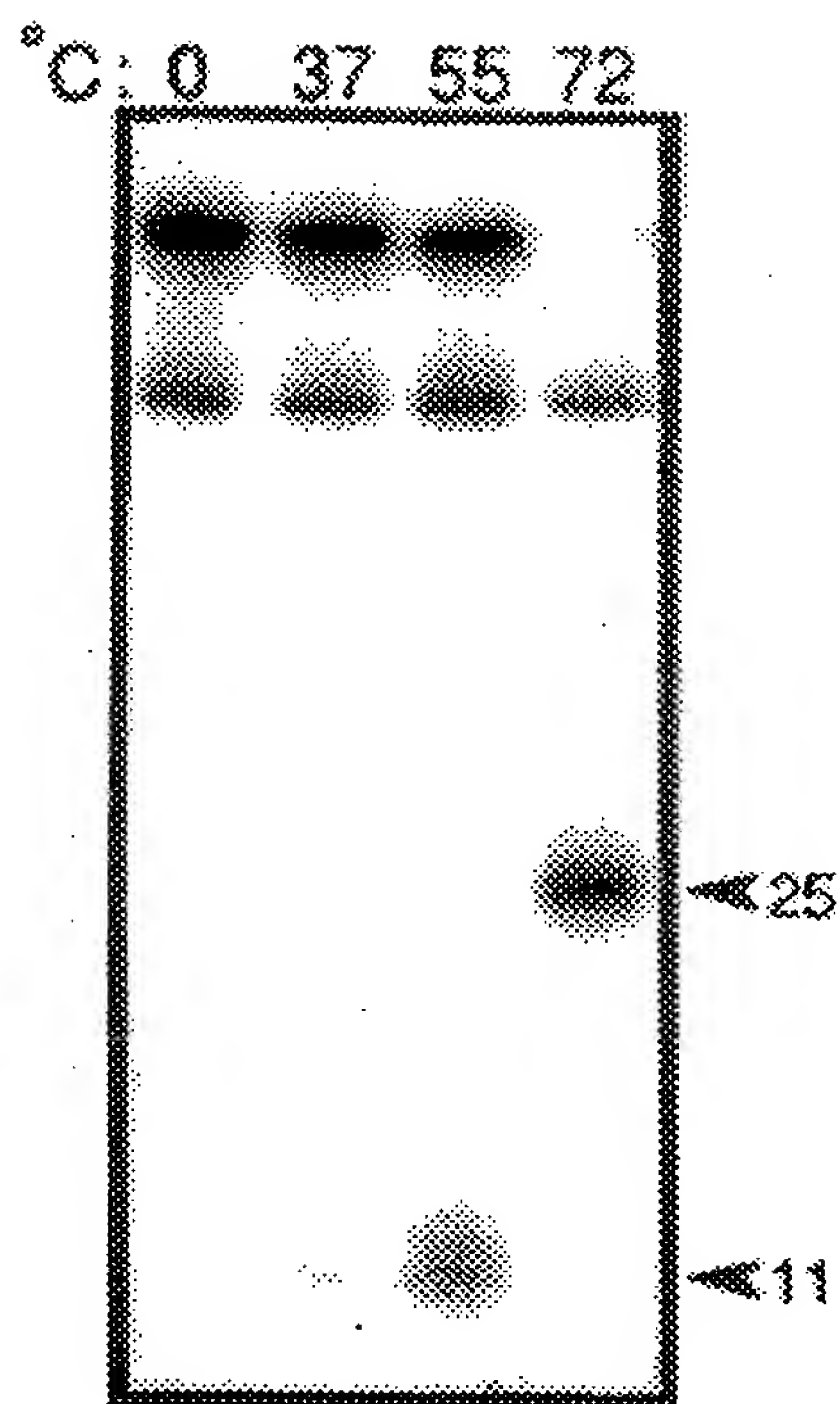


FIG. 9B

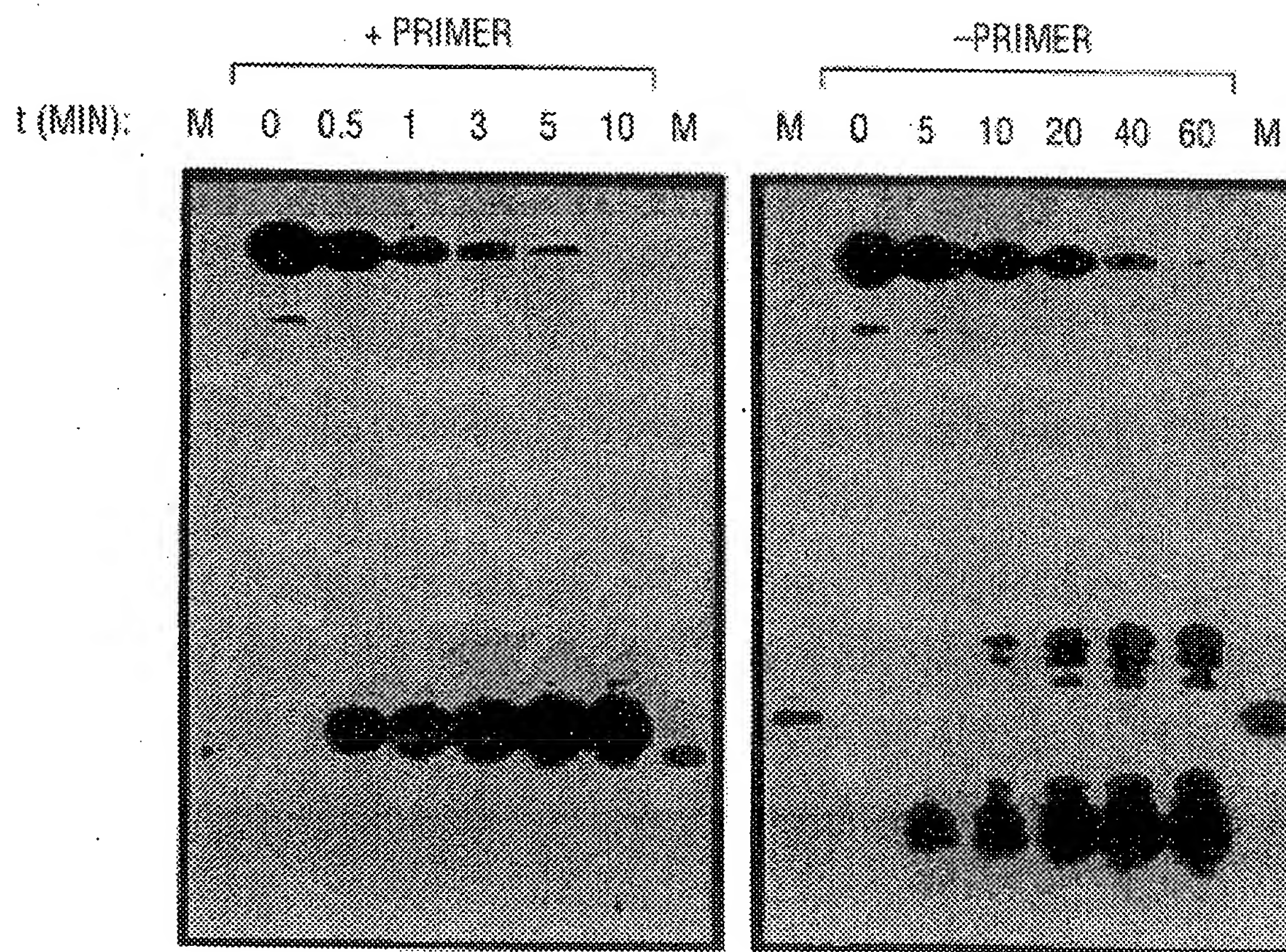


FIG. 10A

FIG. 10B

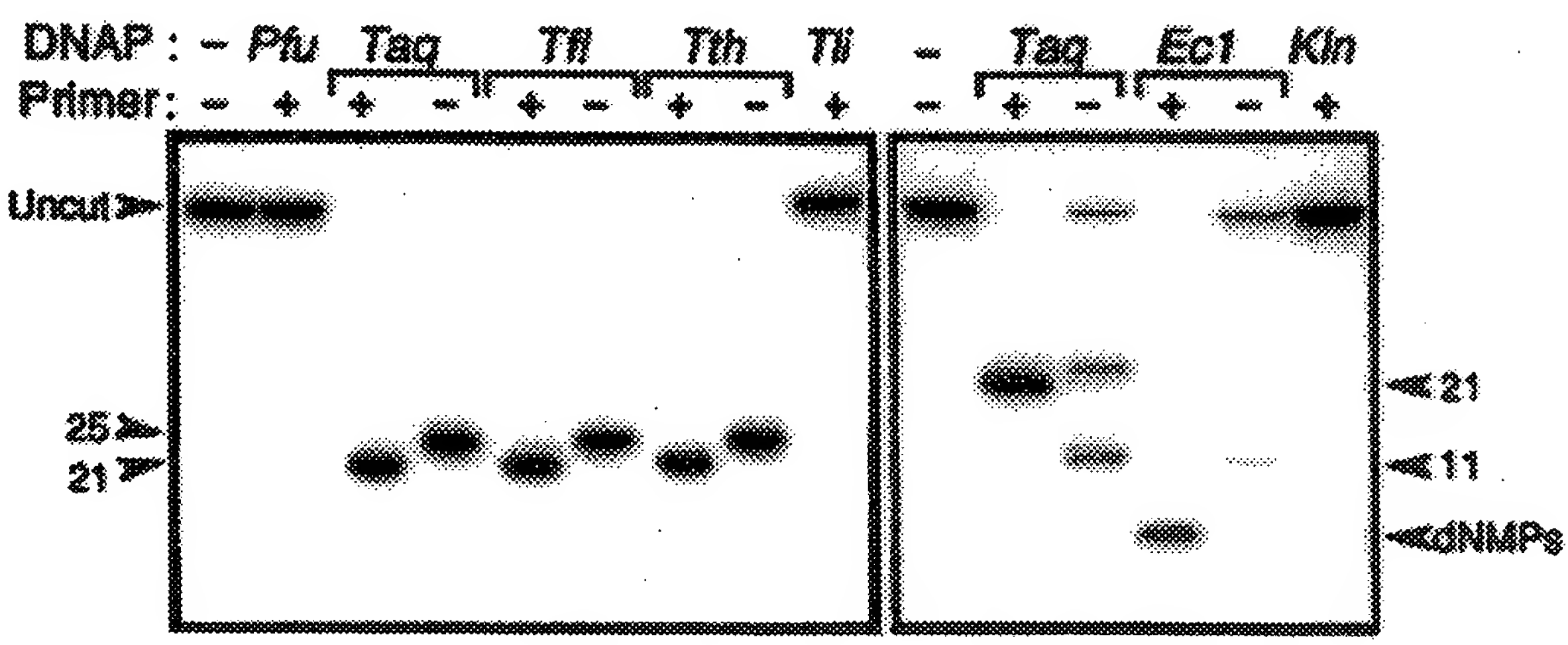
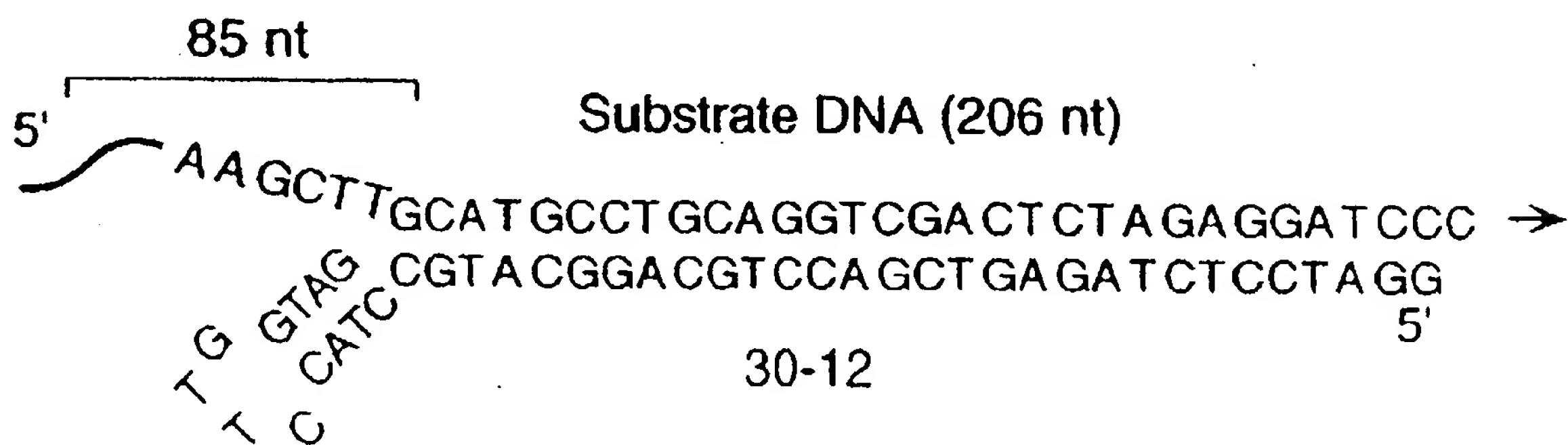
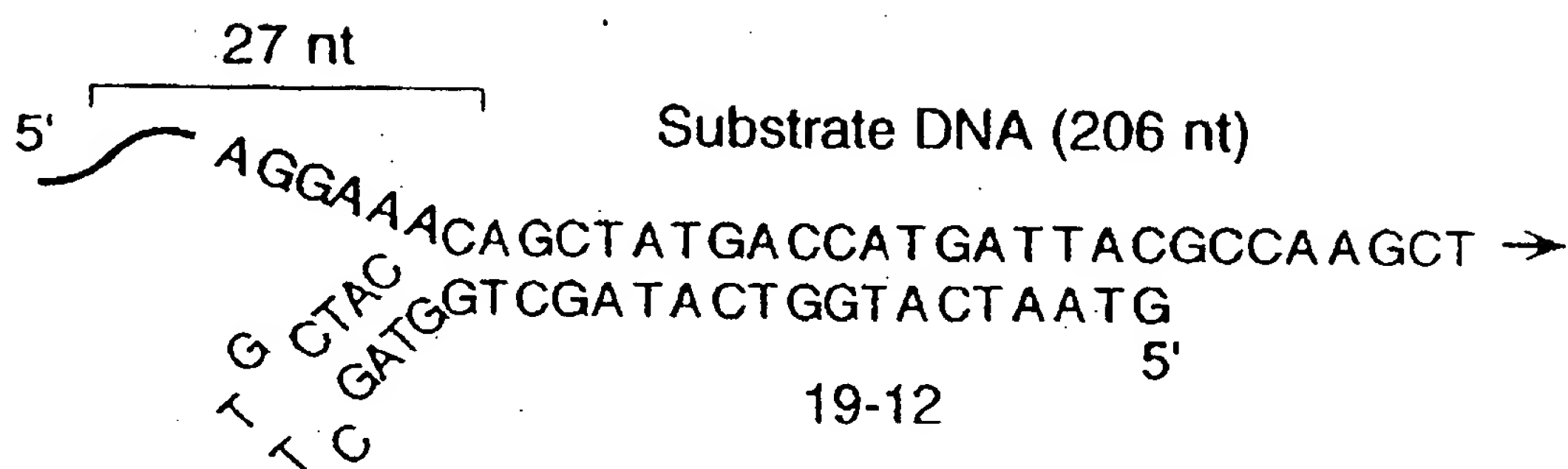


FIG. 11B



FIG. 12A



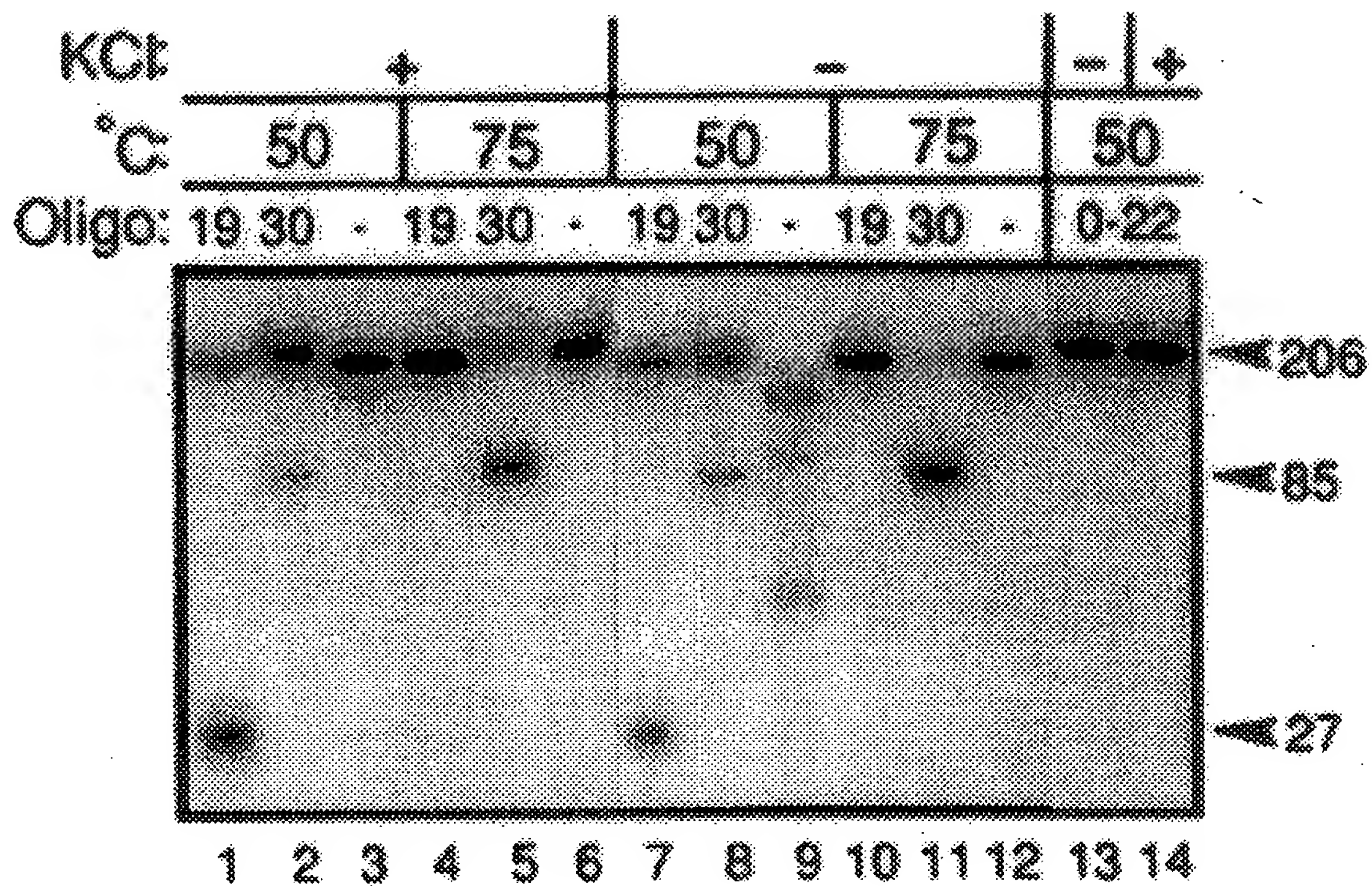


FIG. 12B

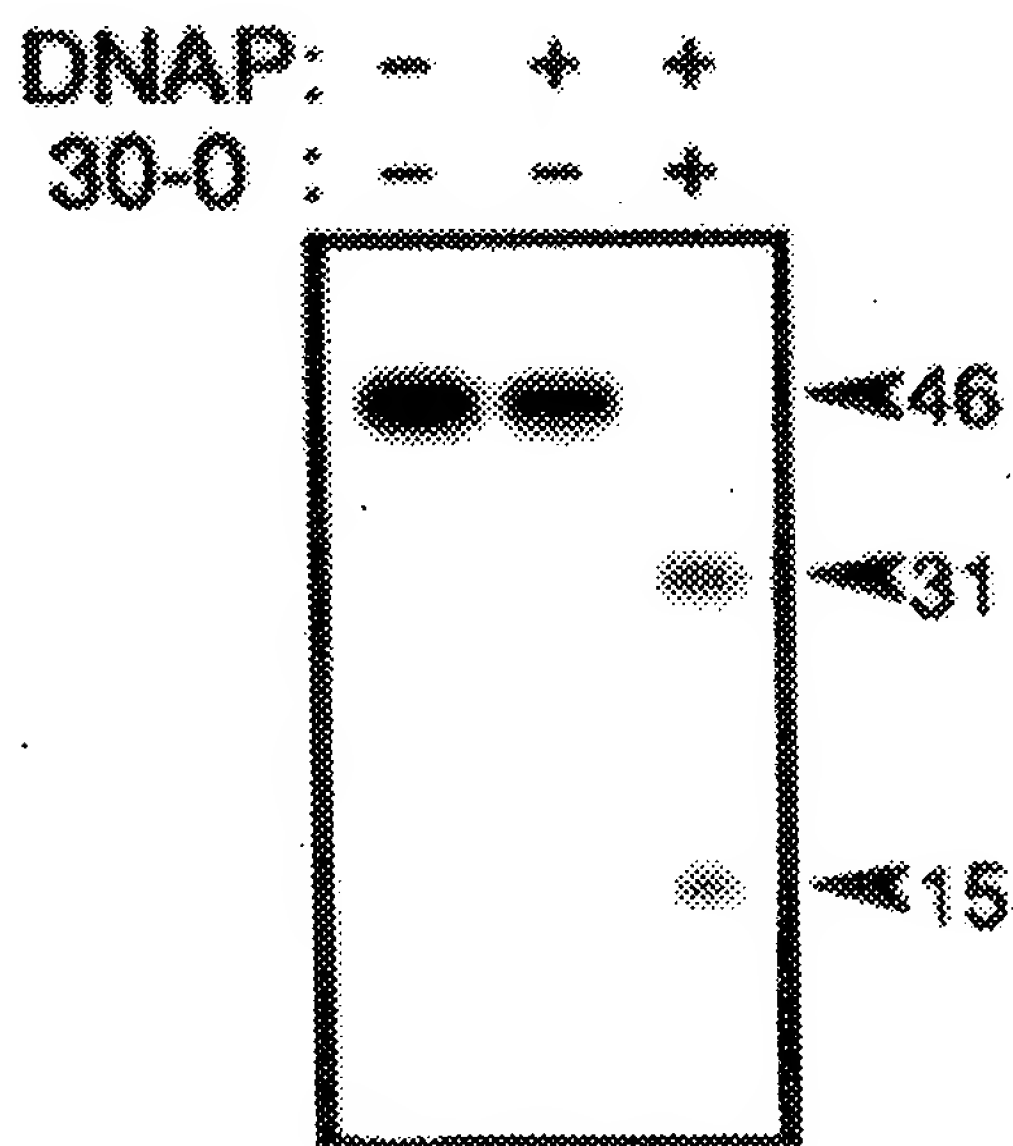


FIG. 13B

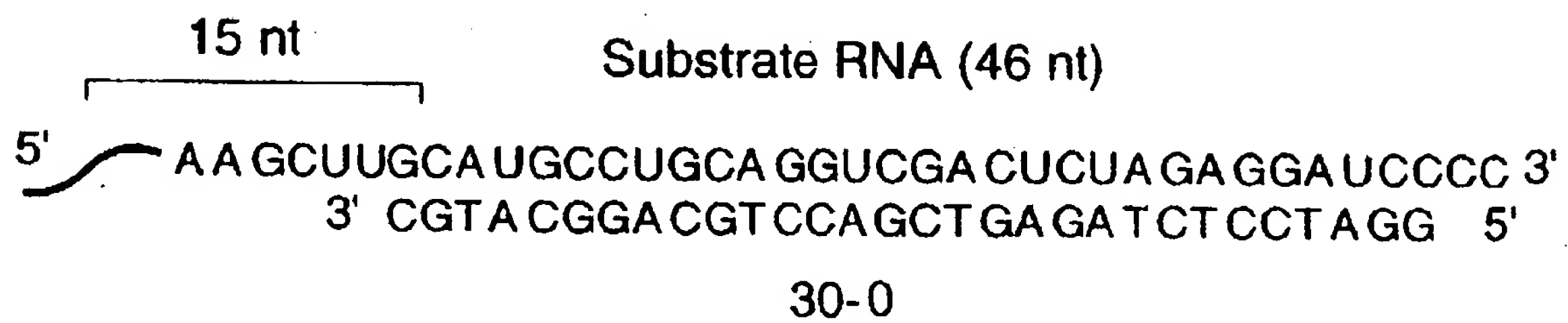


FIG. 13A

-35
TTGACAATTAAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCG
-10
MetAsnSer...
ATGAATTTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC
EcoRI KpnI BamHI Sall PstI HindIII
SstI SmaI XbaI

FIG. 14B

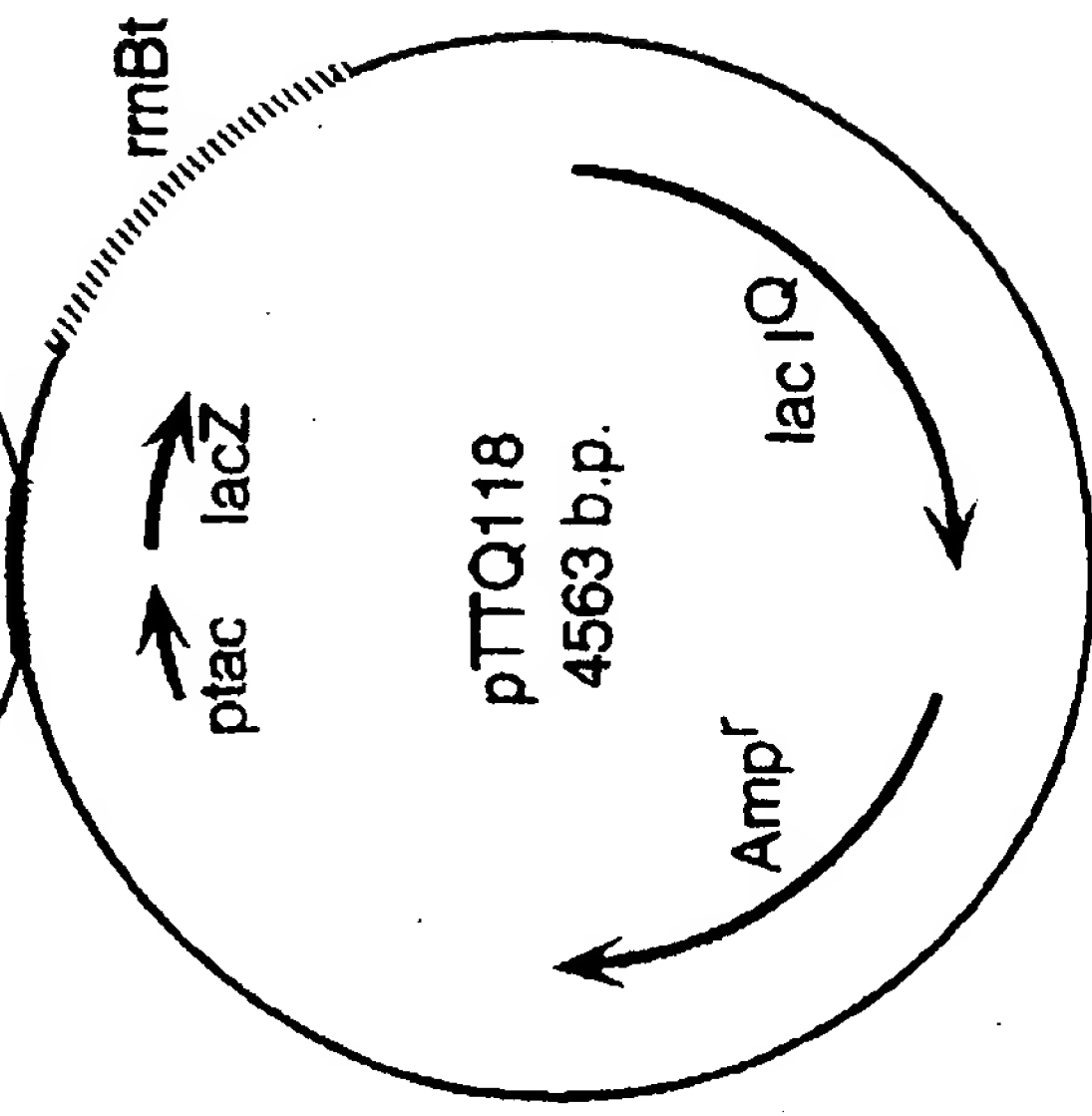
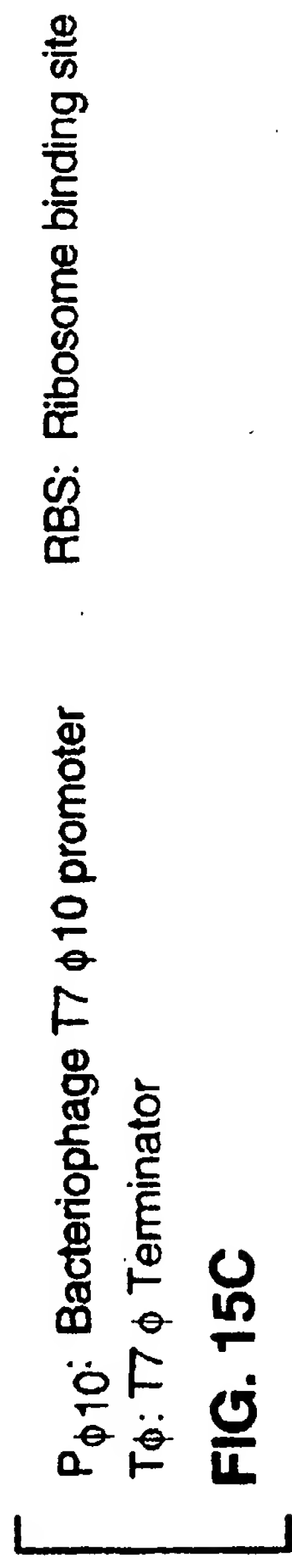
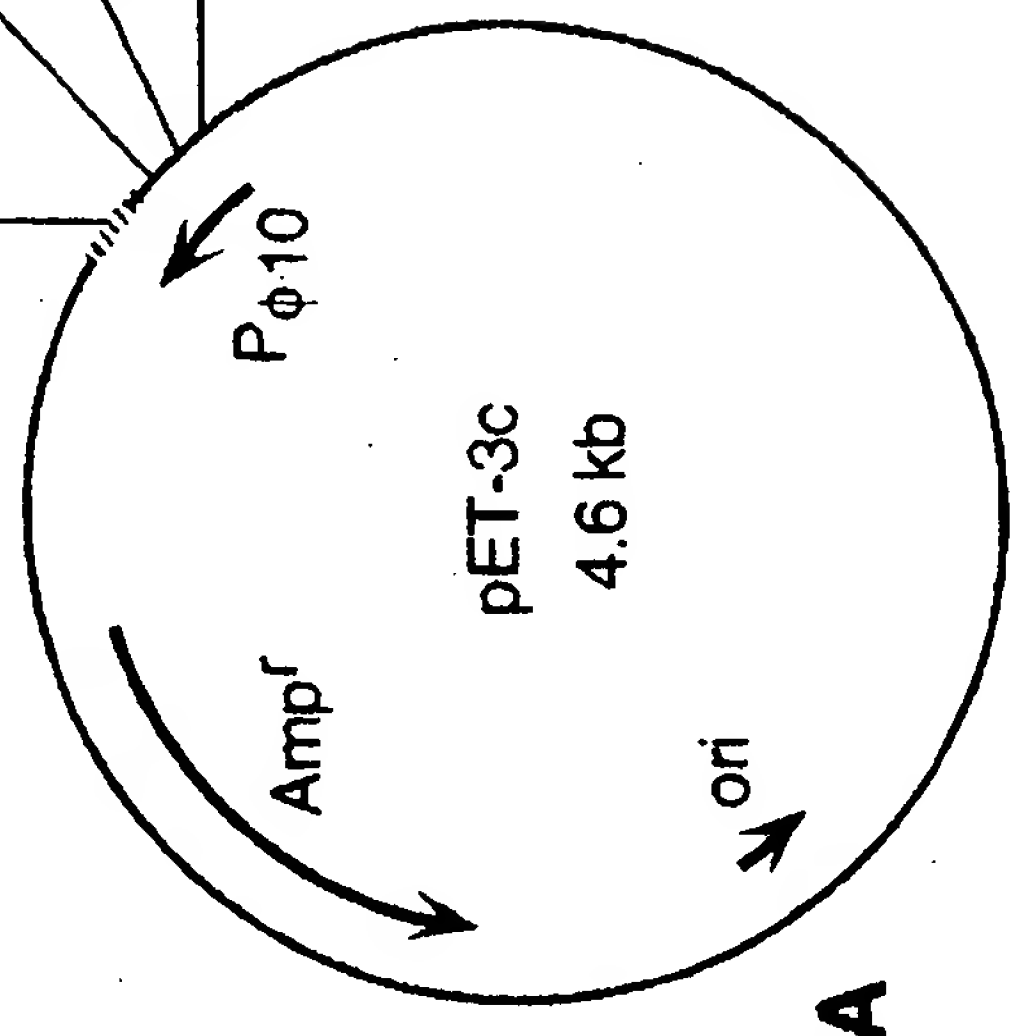
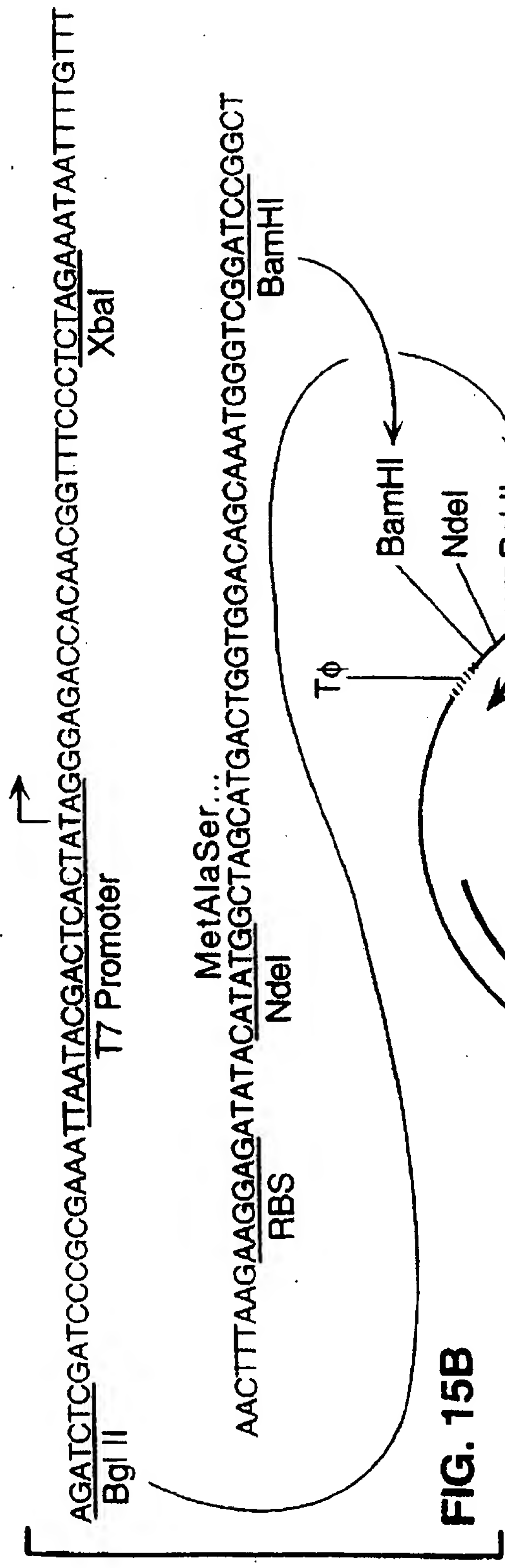


FIG. 14A

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lacIQ: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rmBt: E. coli rmB transcription terminator

FIG. 14C



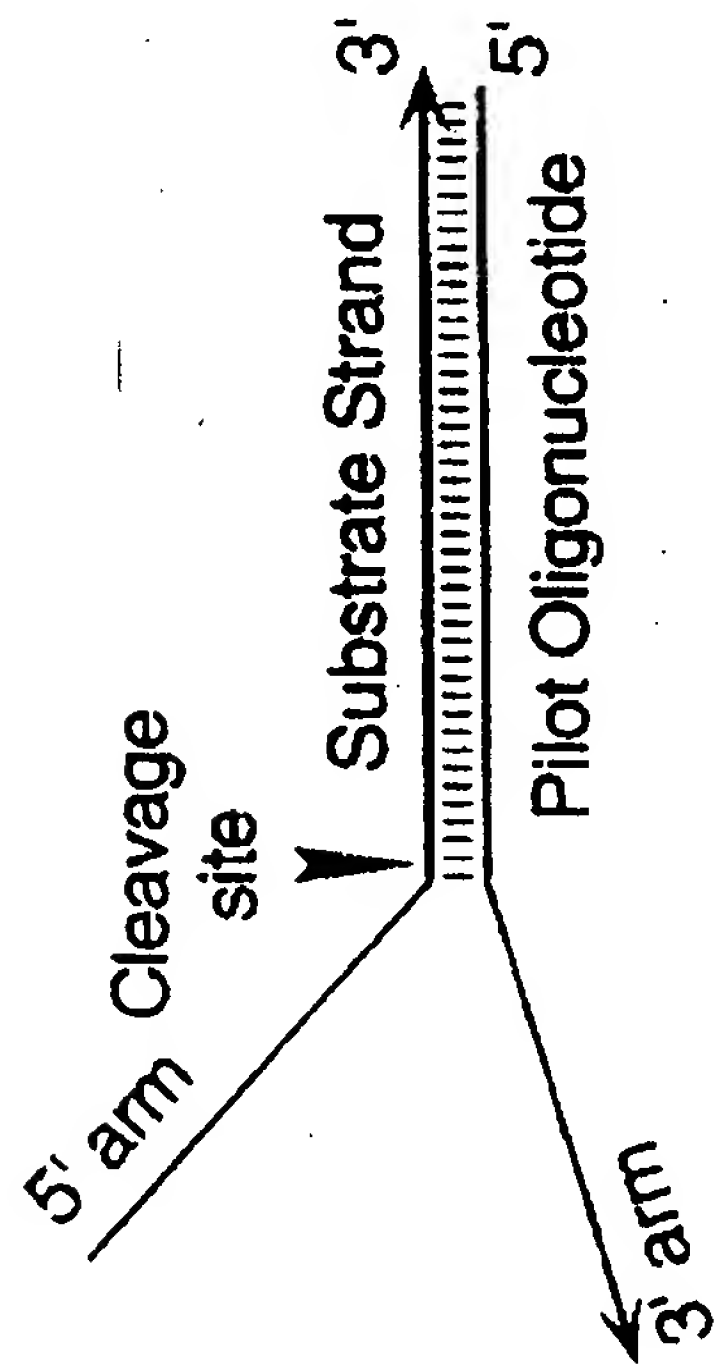


FIG. 16A

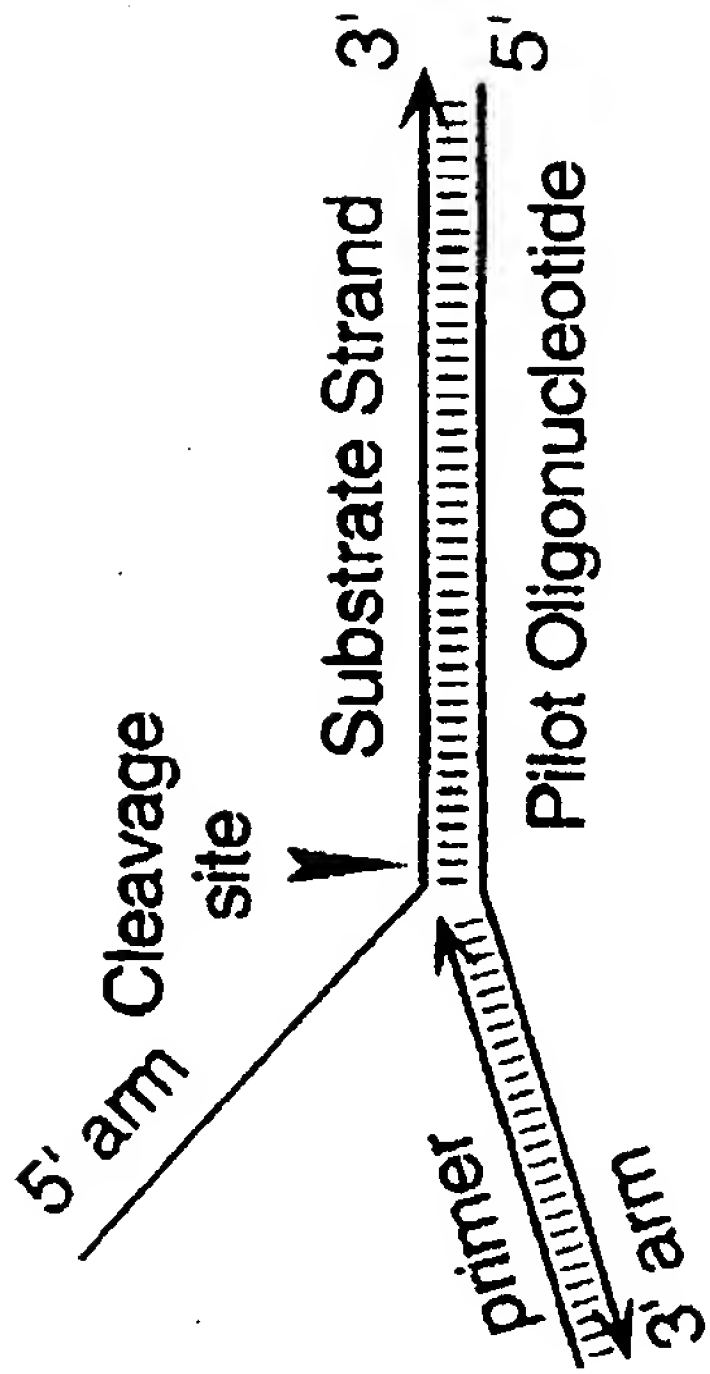


FIG. 16B

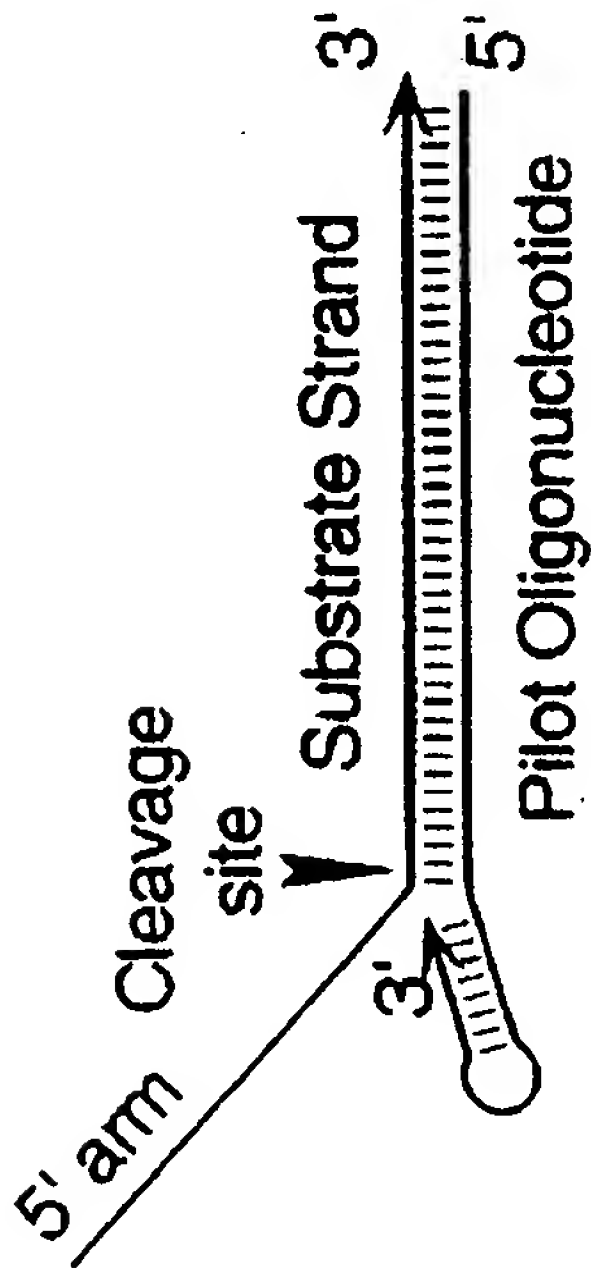


FIG. 16C

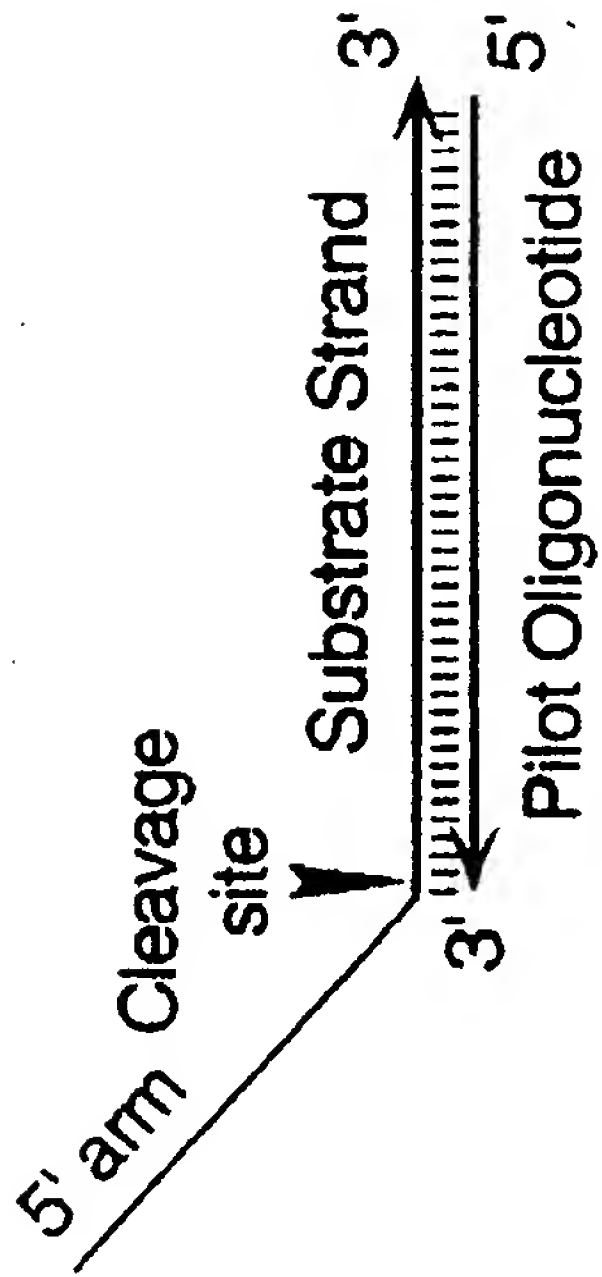


FIG. 16D

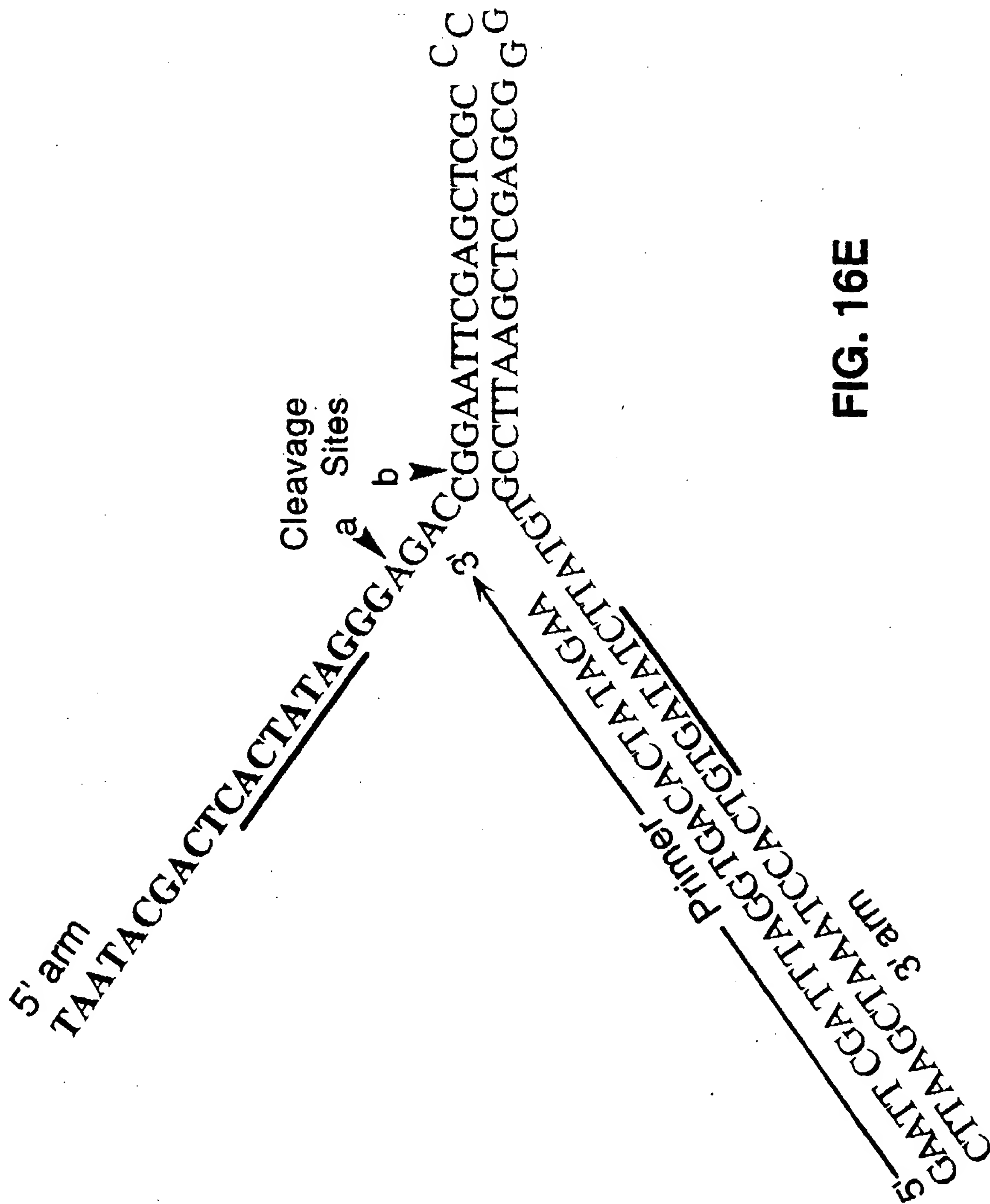
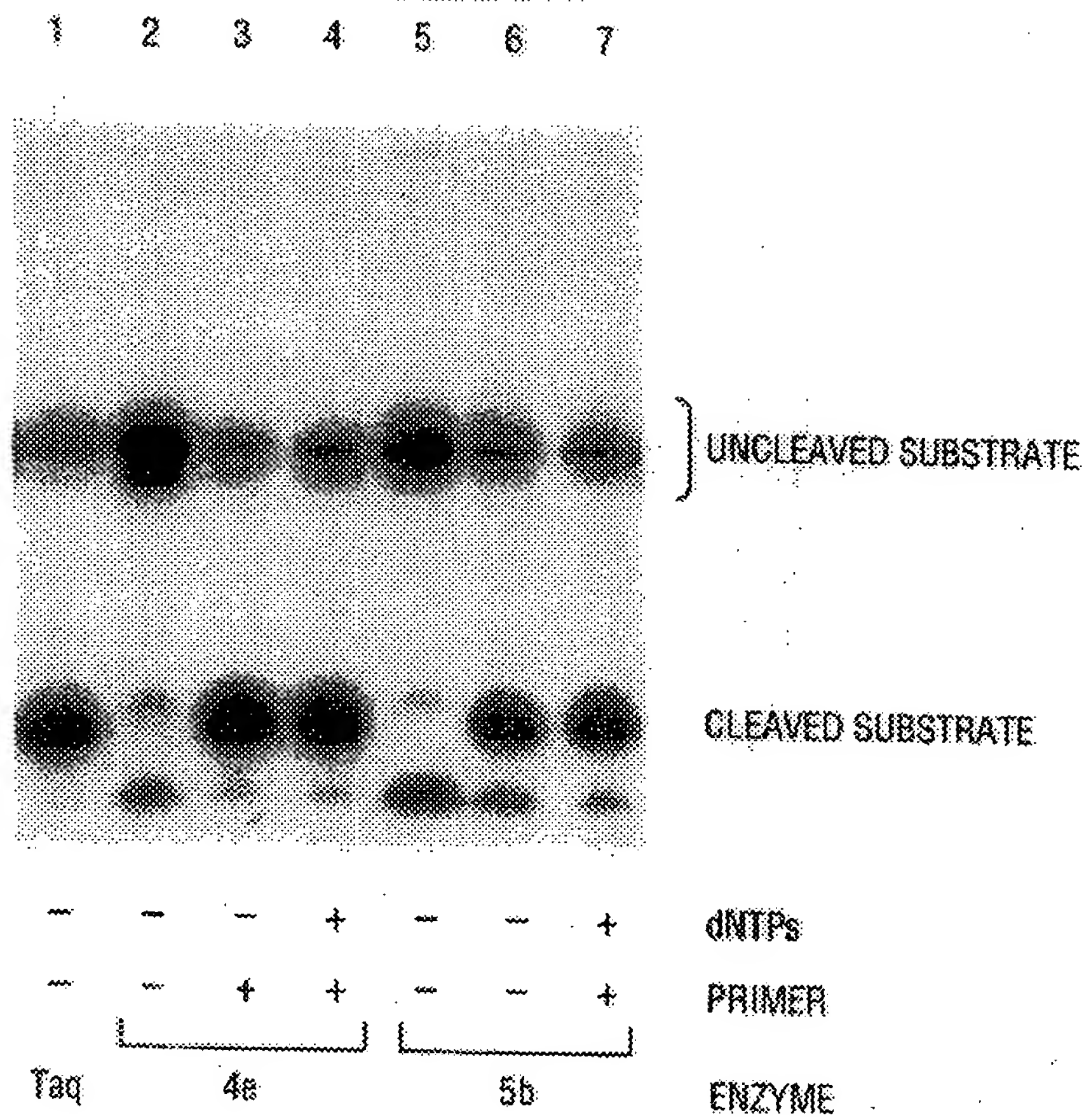


FIG. 16E



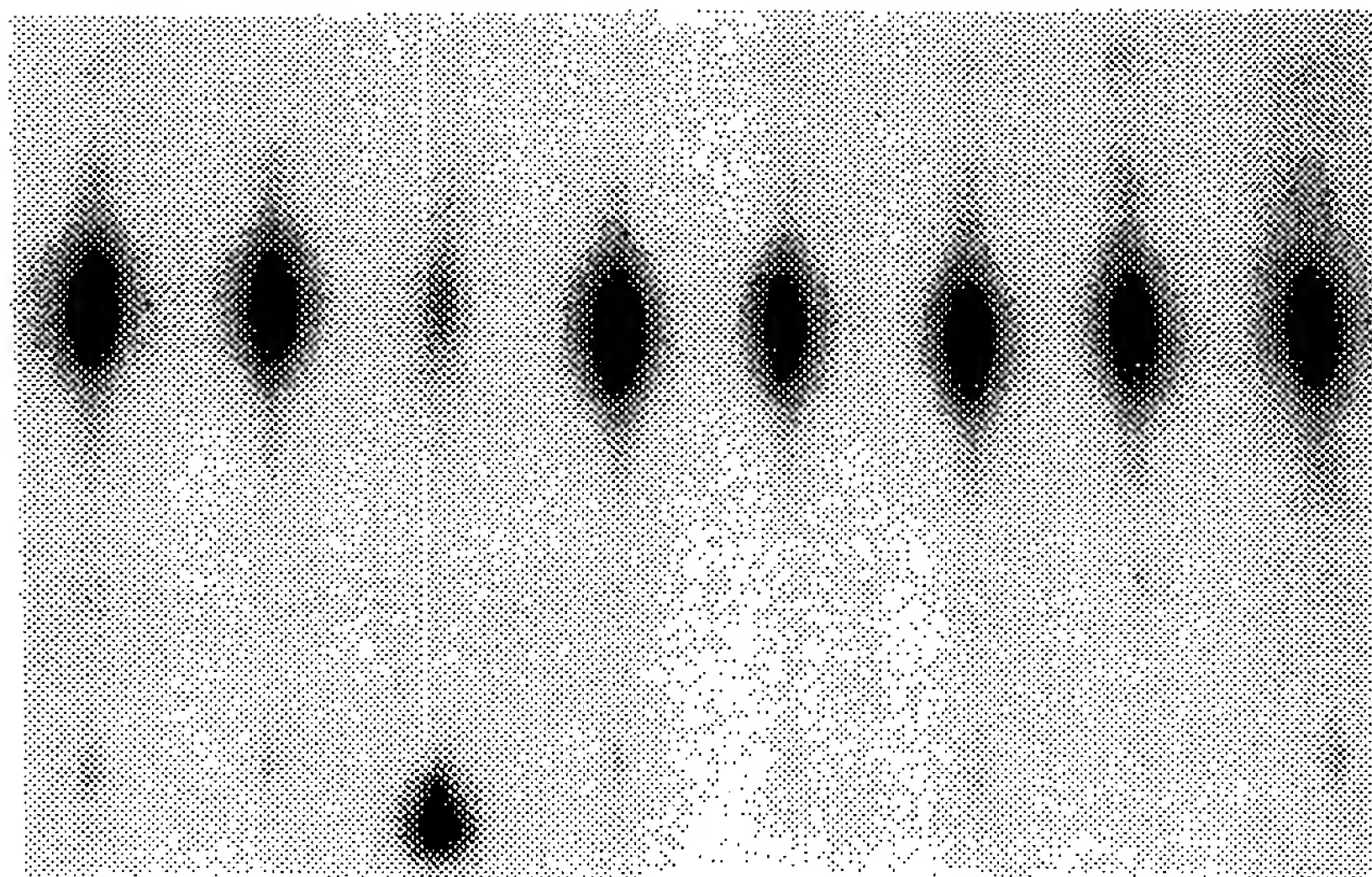
FIG. 17





UNINCORPORATED
 ^{32}P dCTP →

INCORPORATED
 ^{32}P dCMP →



ENZYME	Taq	—	Taq	4b	4c	4d	4e	4f
PRIMED M13	—	+	+	+	+	+	+	+

FIG. 18

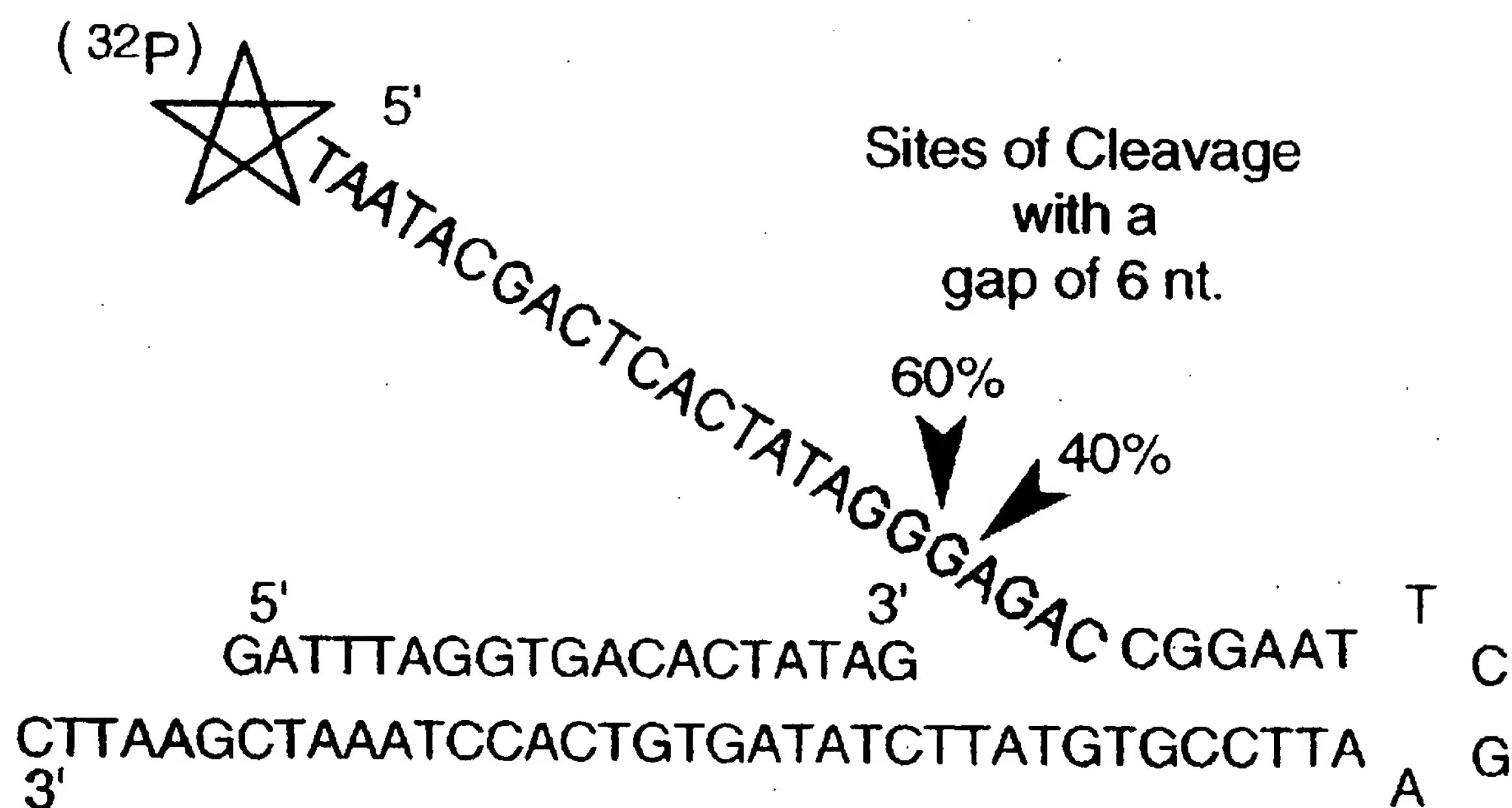


FIG. 19A

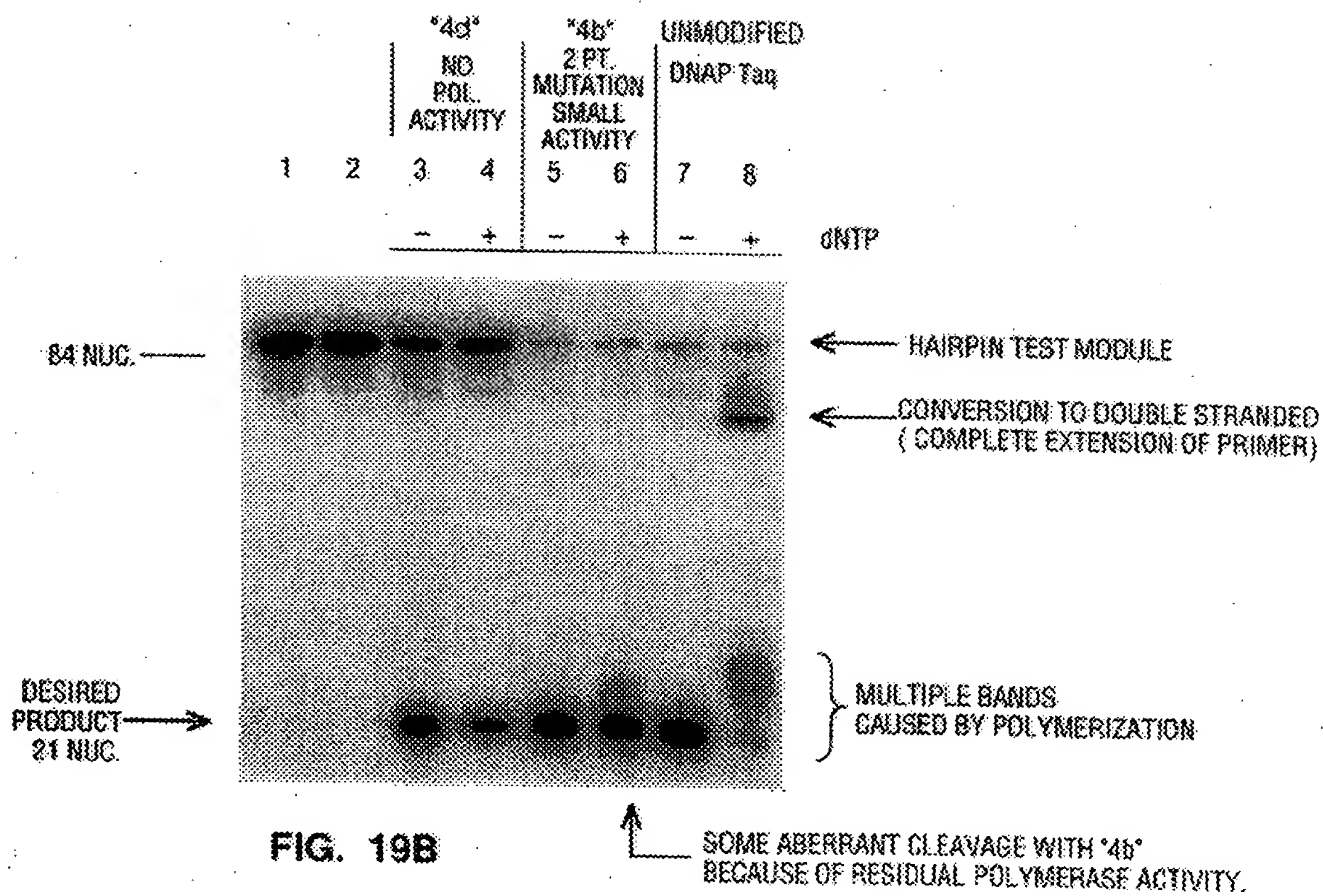


FIG. 19B

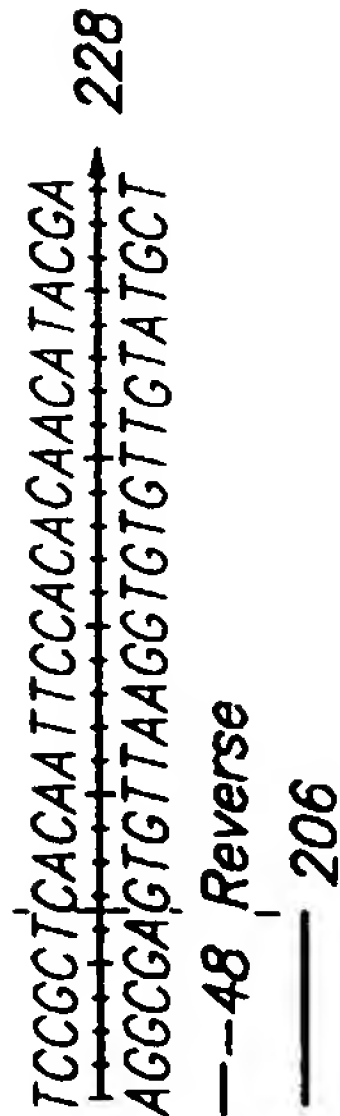
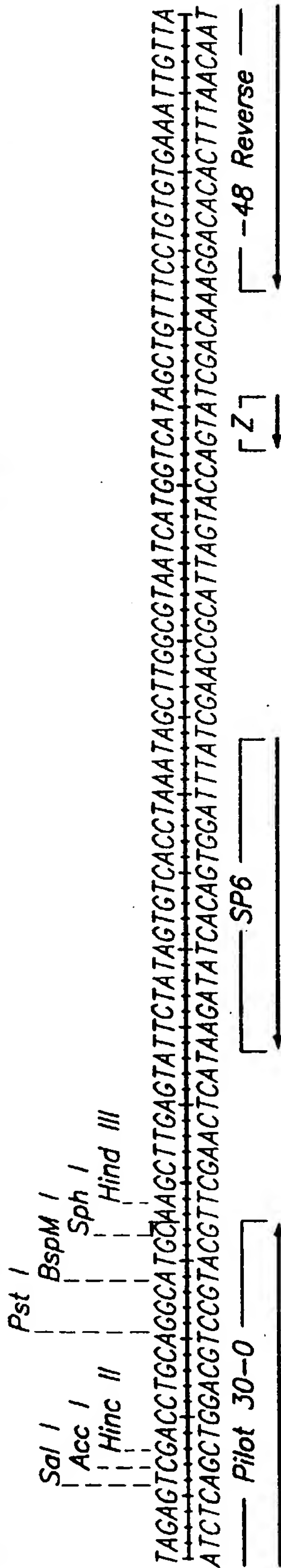
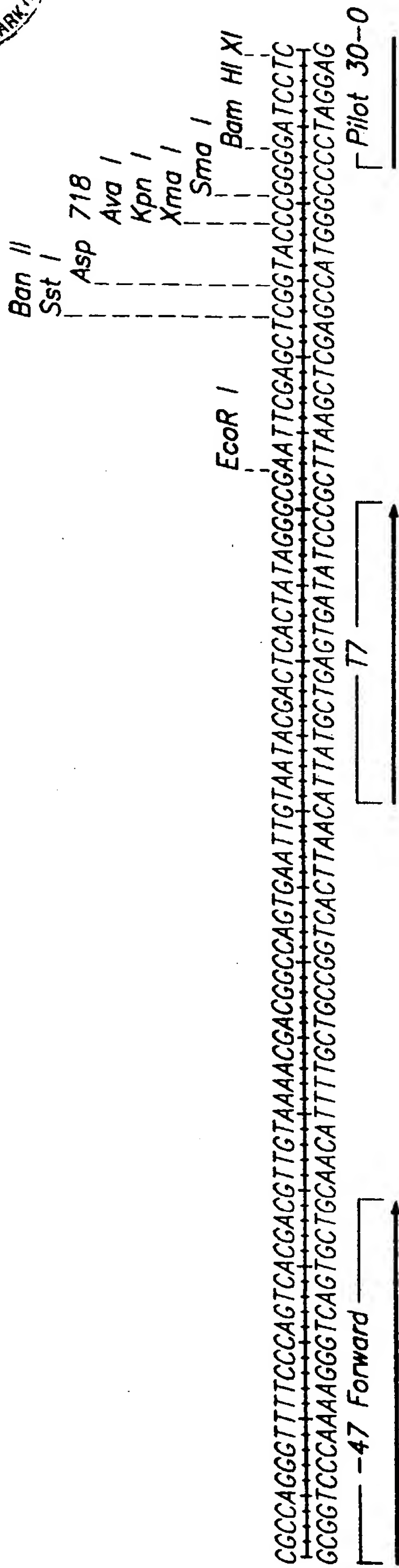


FIG. 21

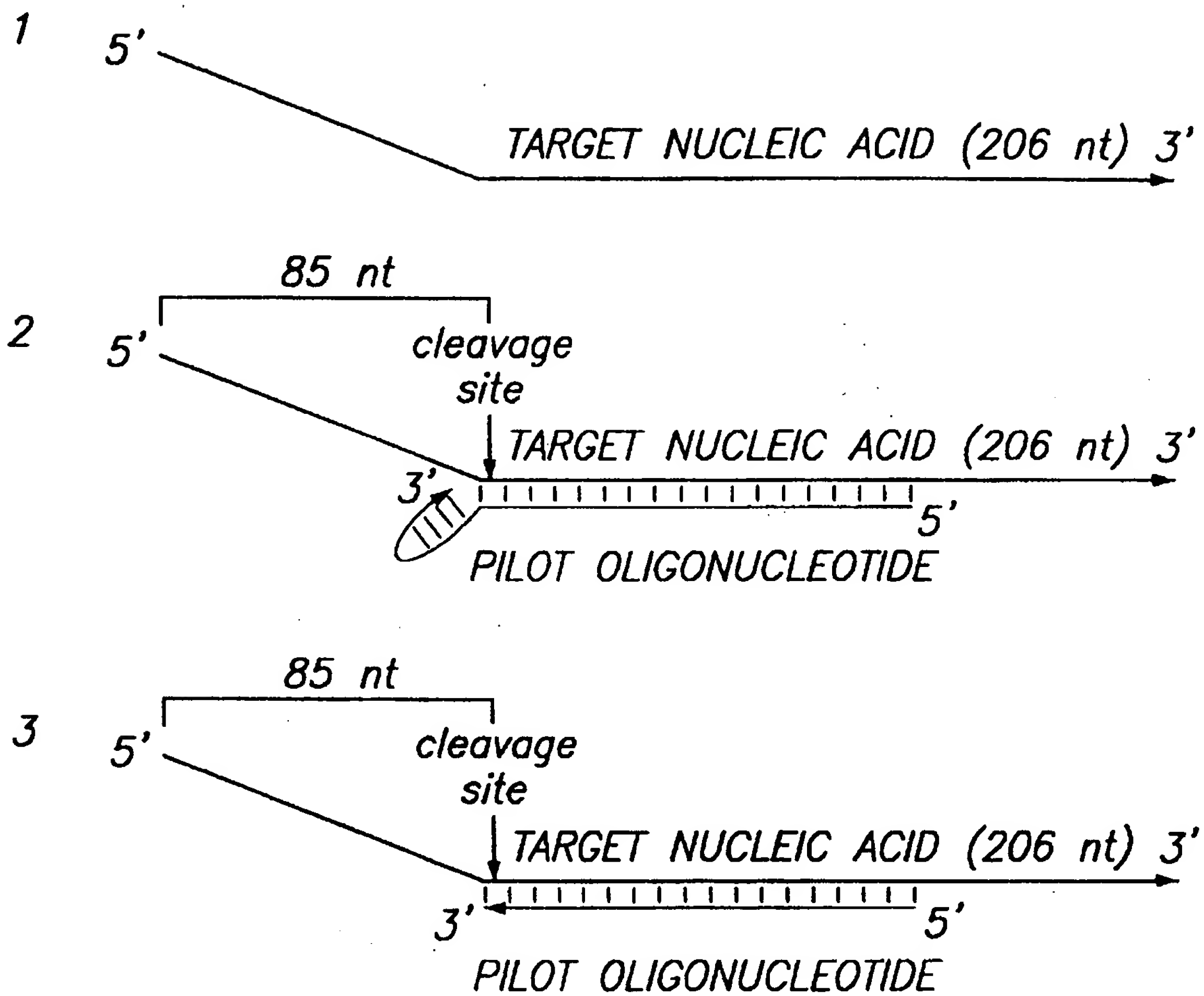


FIG. 22A

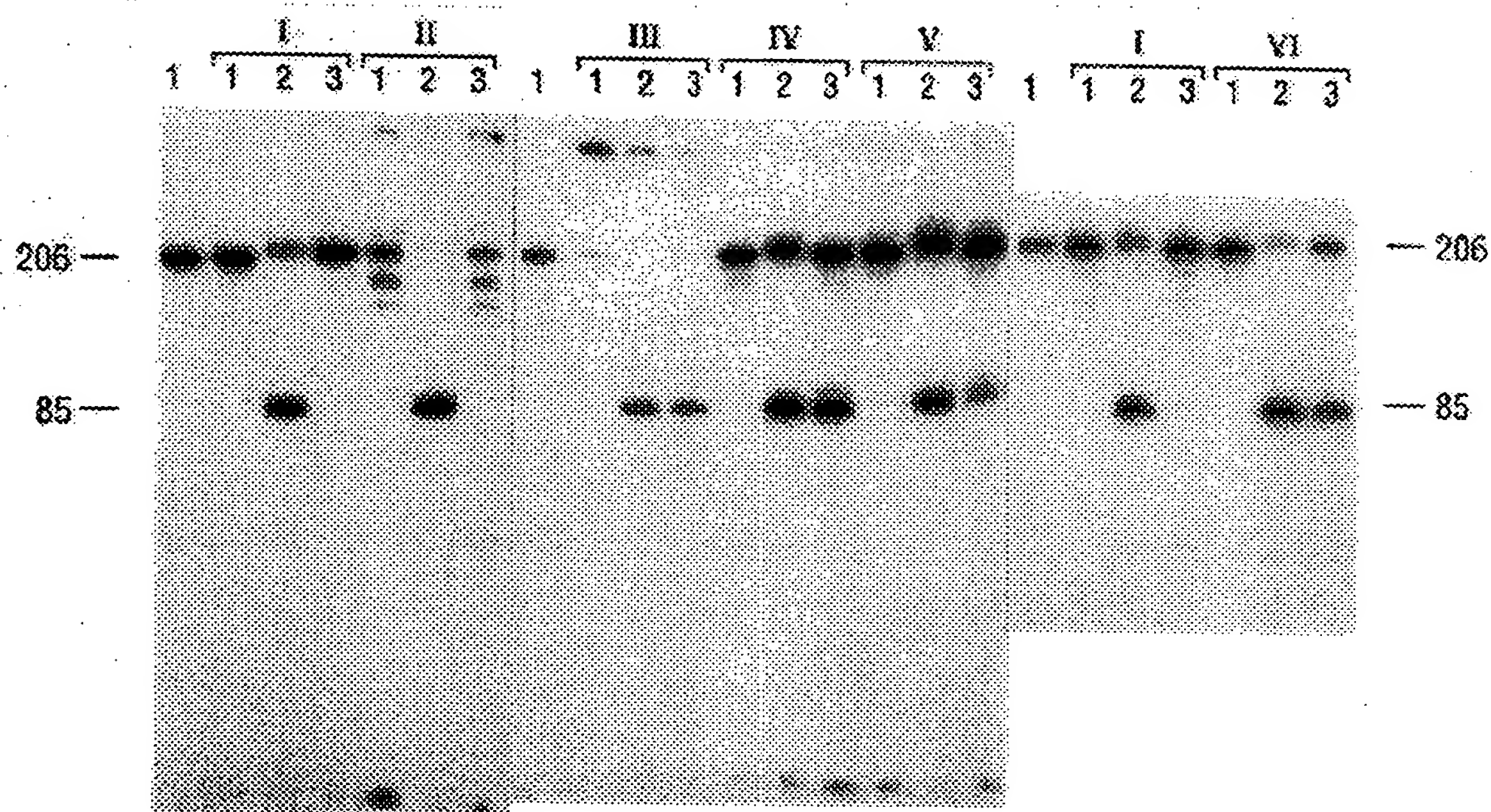


FIG. 22B

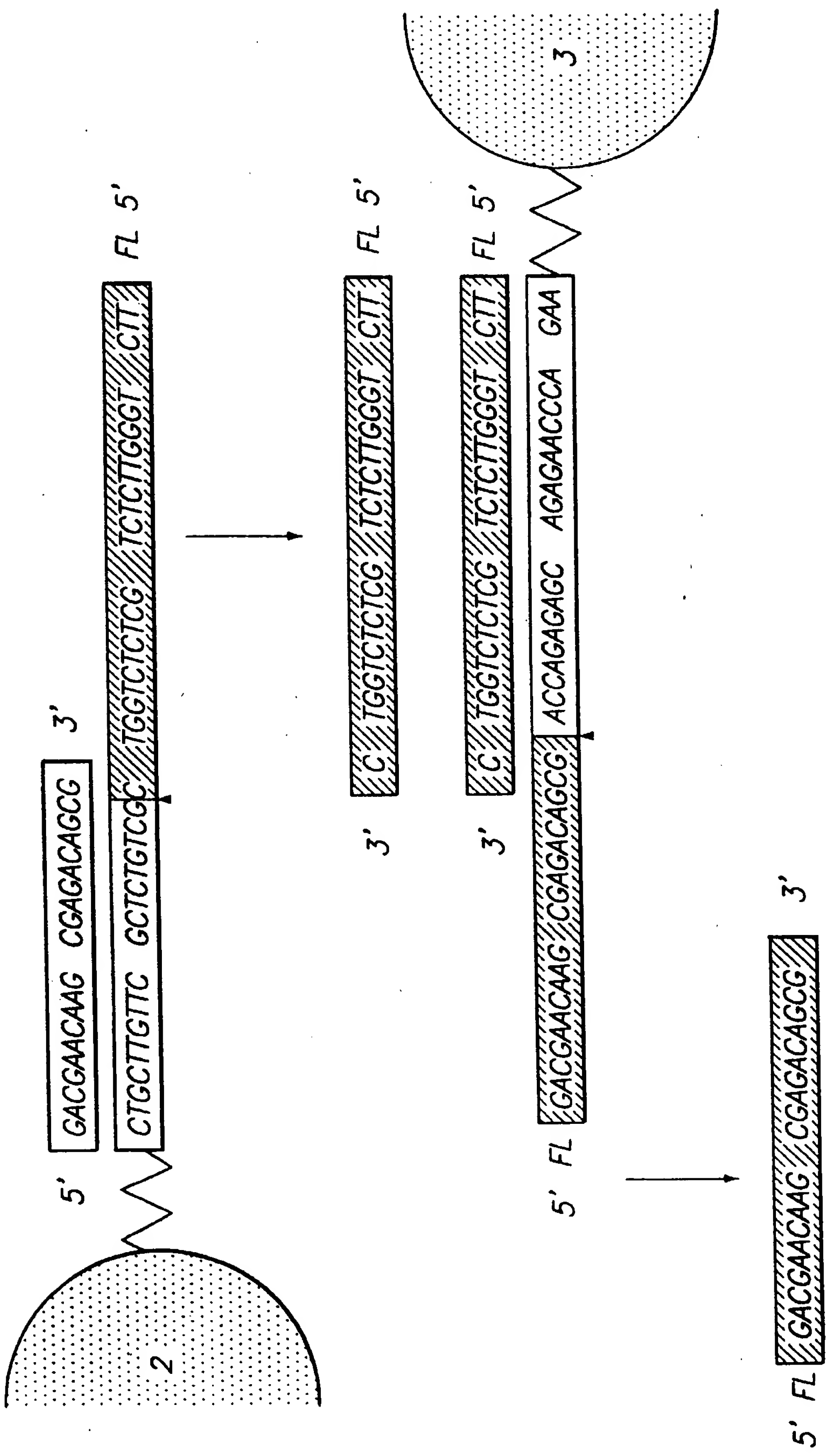
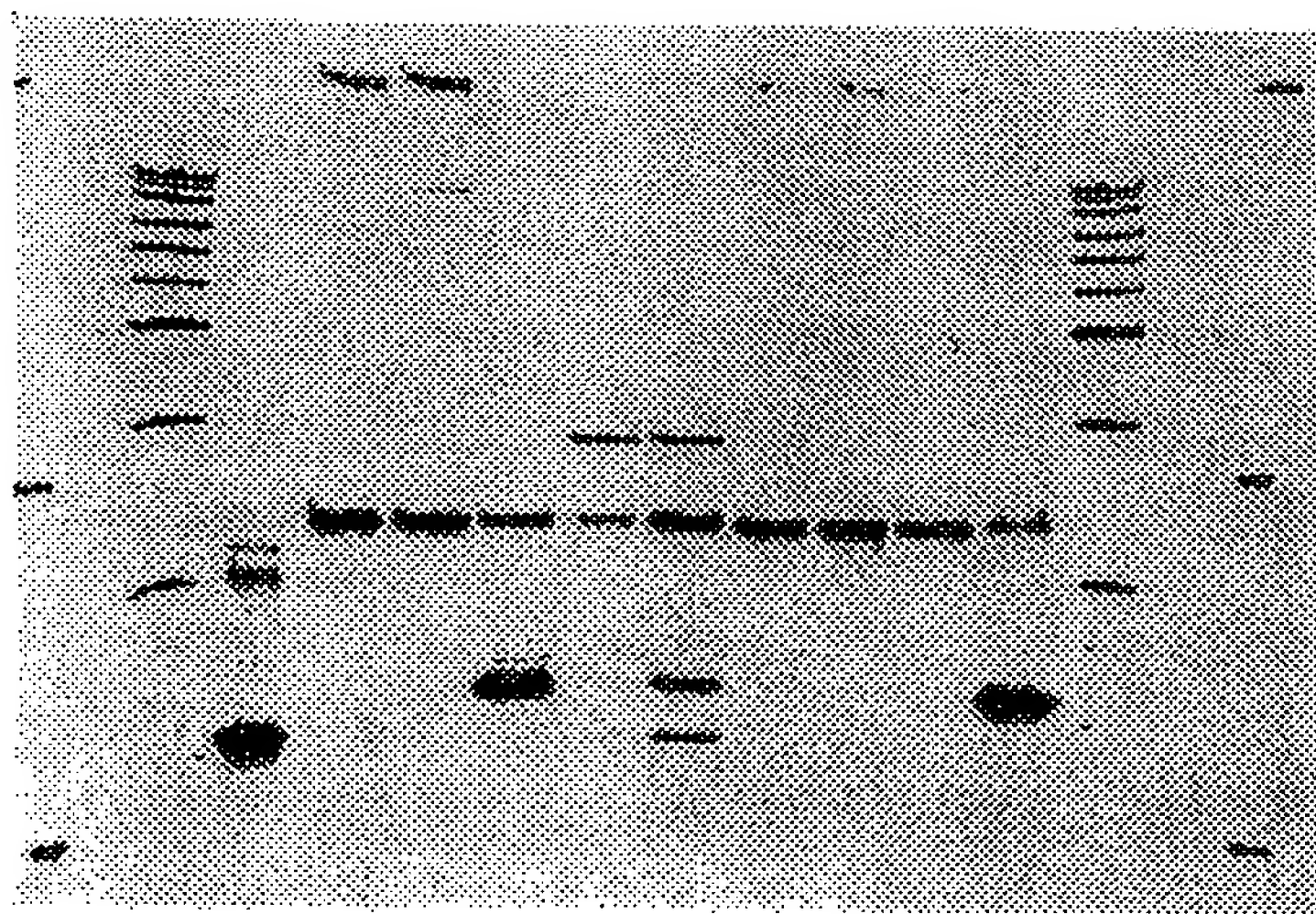


FIG. 23



CDR BEAD			T	T	T	A/T	A/T	A	A	A		
PILOT			-	-	+	-	+	+	-	-		
CLEAVASE	M	M	-	+	+	+	+	+	+	-	M	M

20nt MARKER →



← 24nt MARKER

FIG. 24

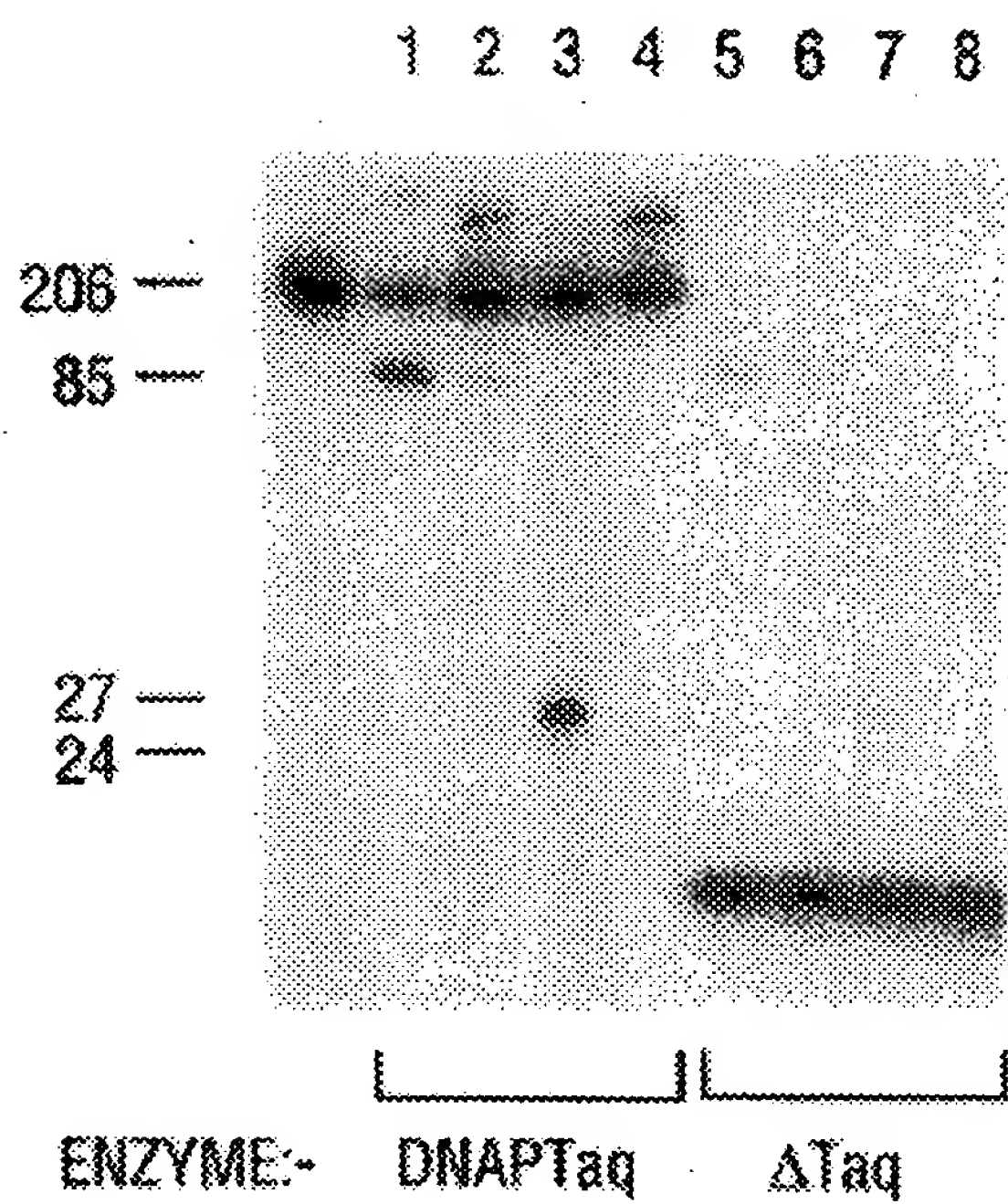


FIG. 25A

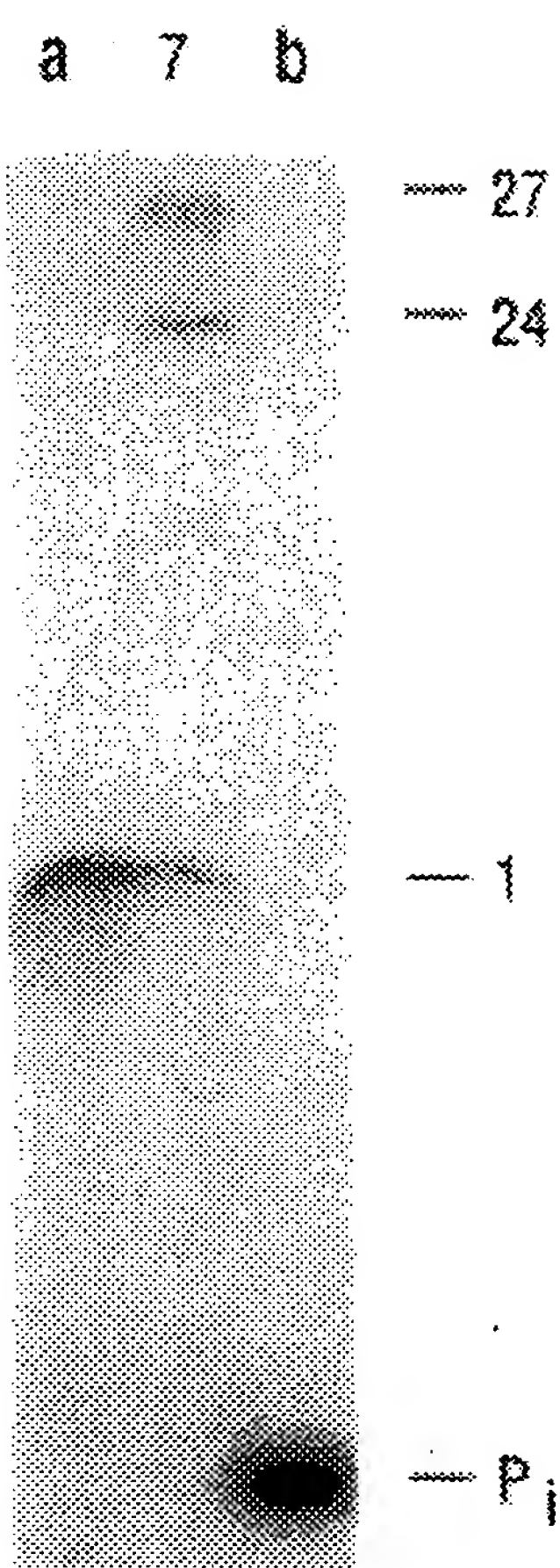


FIG. 25B



FIG. 26A

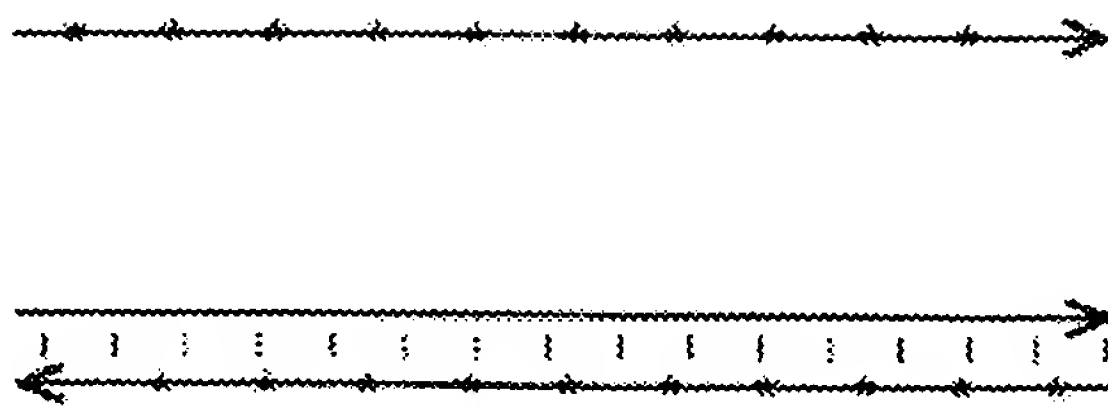
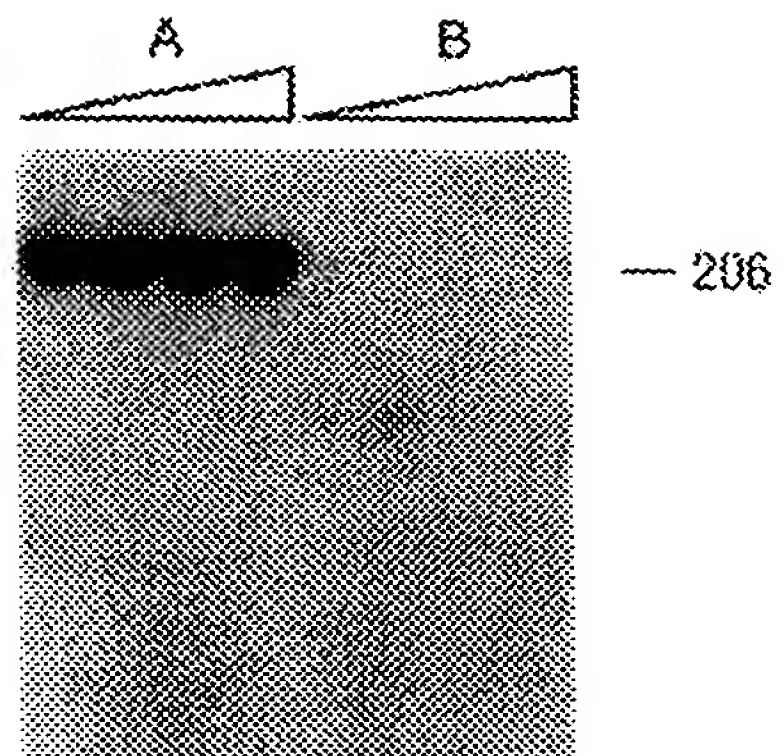


FIG. 26B

* = 32p



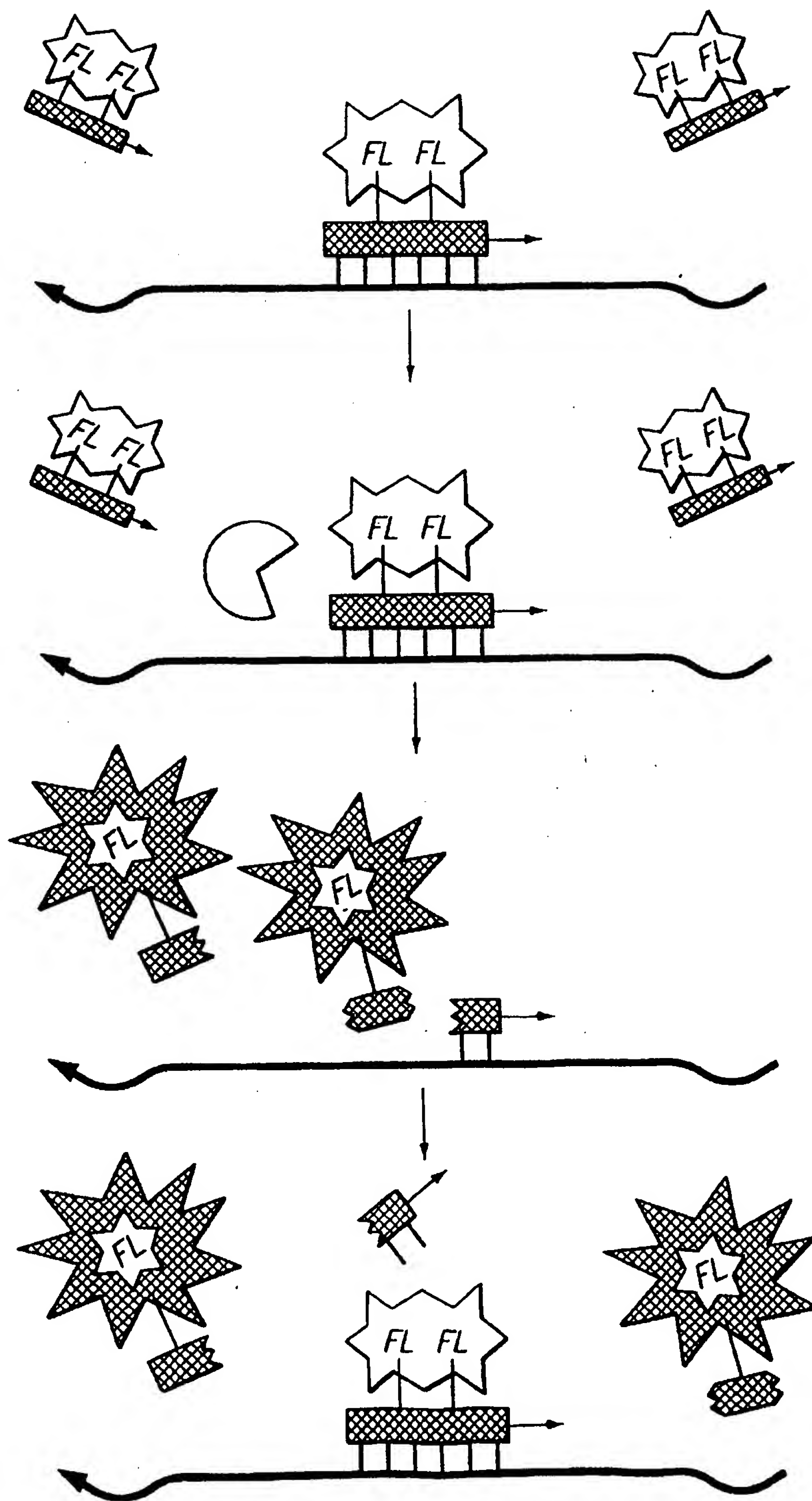


FIG. 27

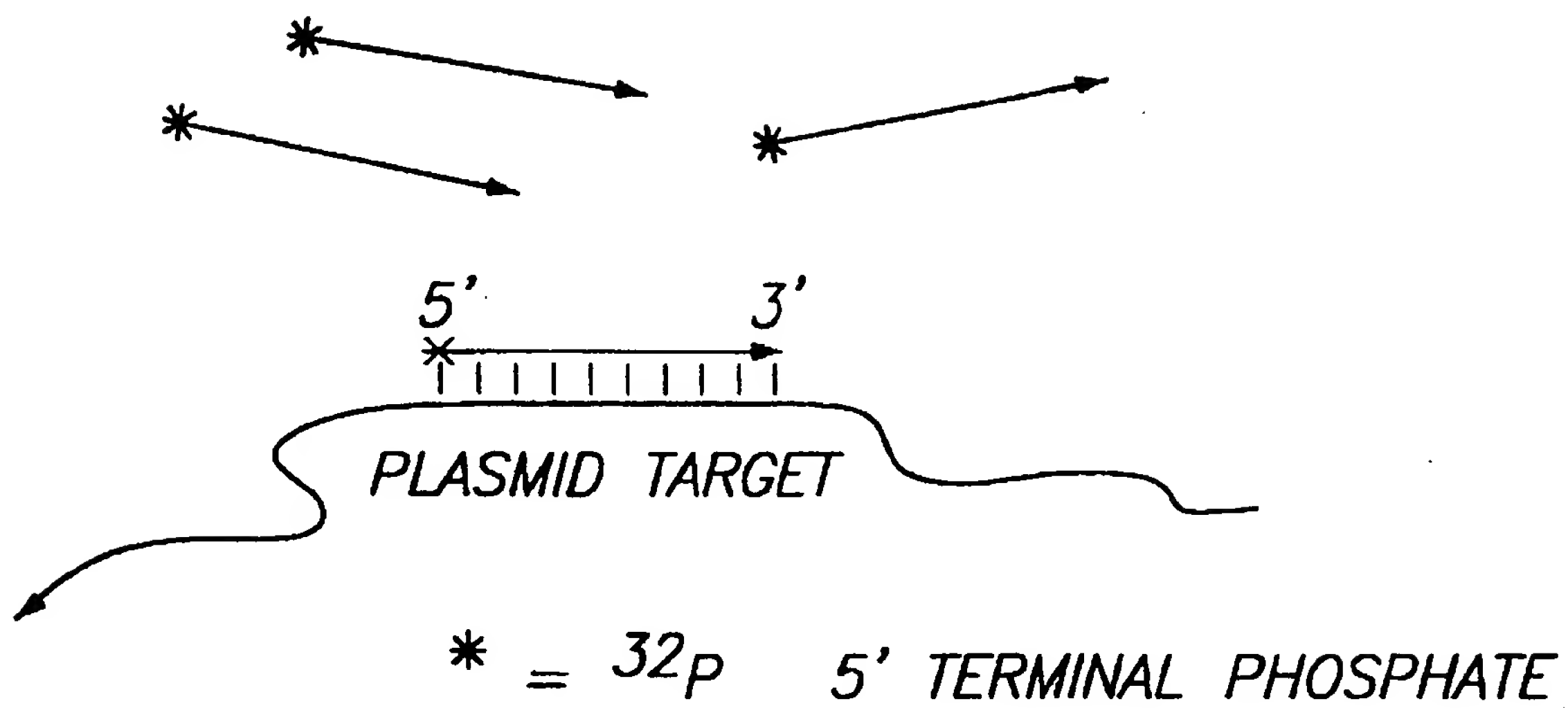


FIG. 28A

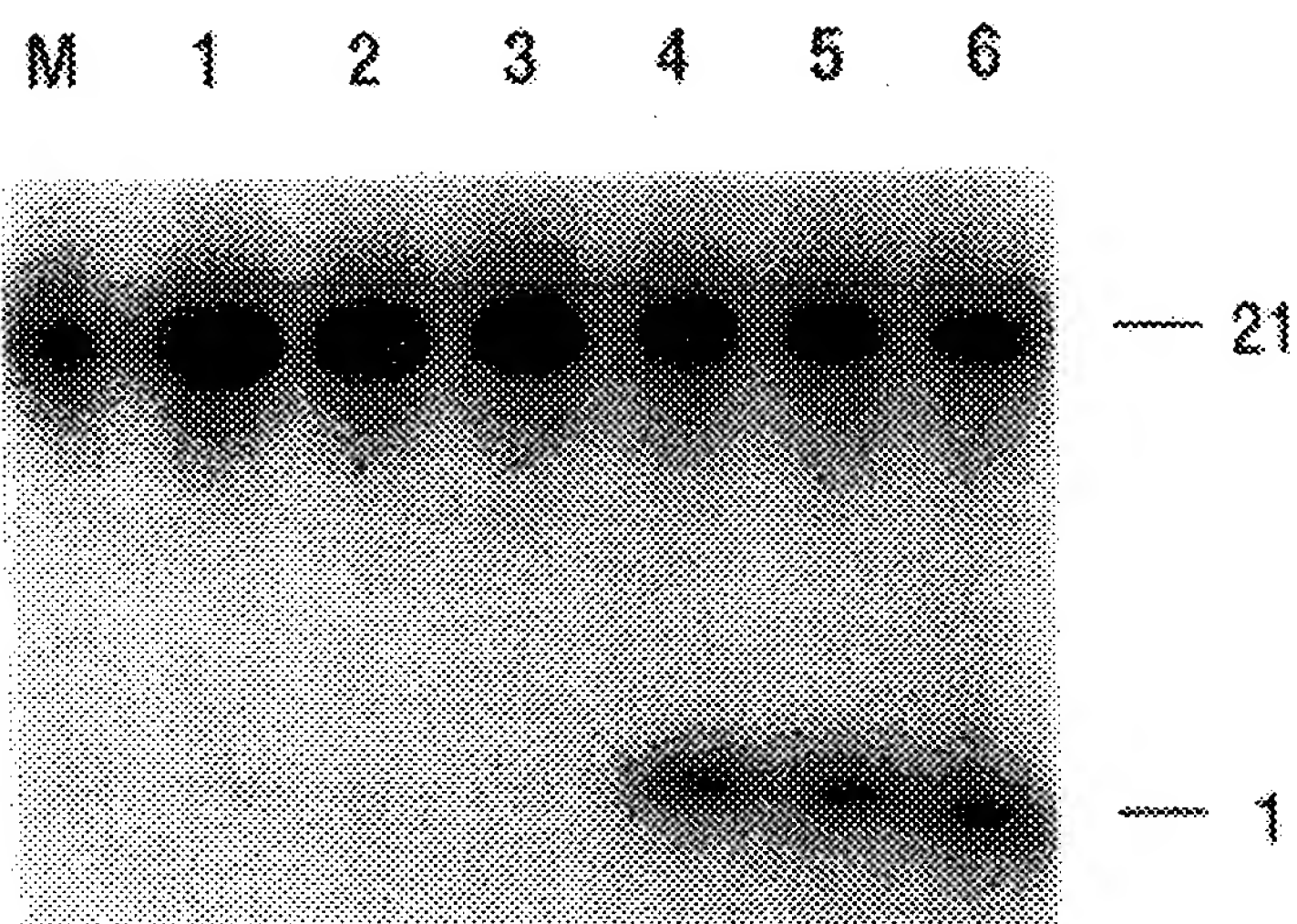
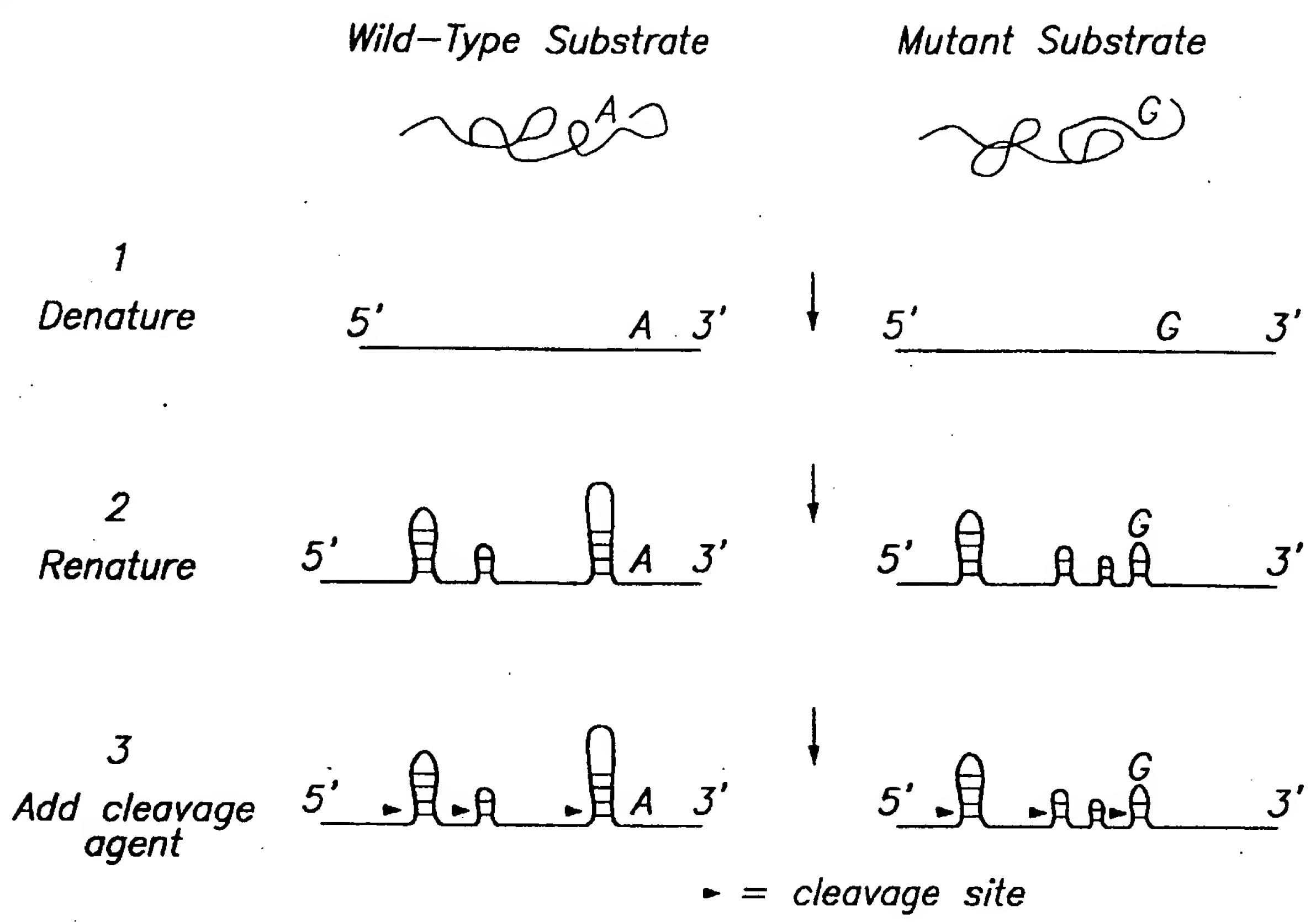


FIG. 28B



4
Resolve reaction products

5
Detect unique cleavage "fingerprint"

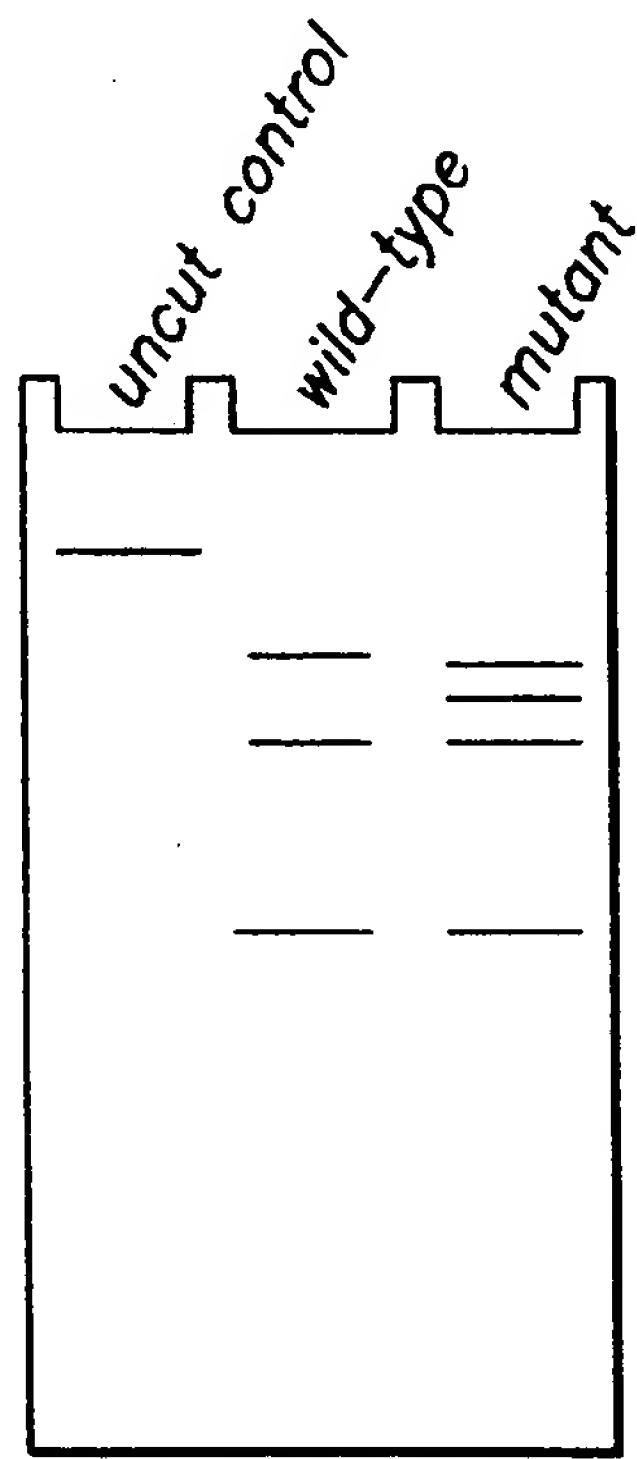


FIG. 29

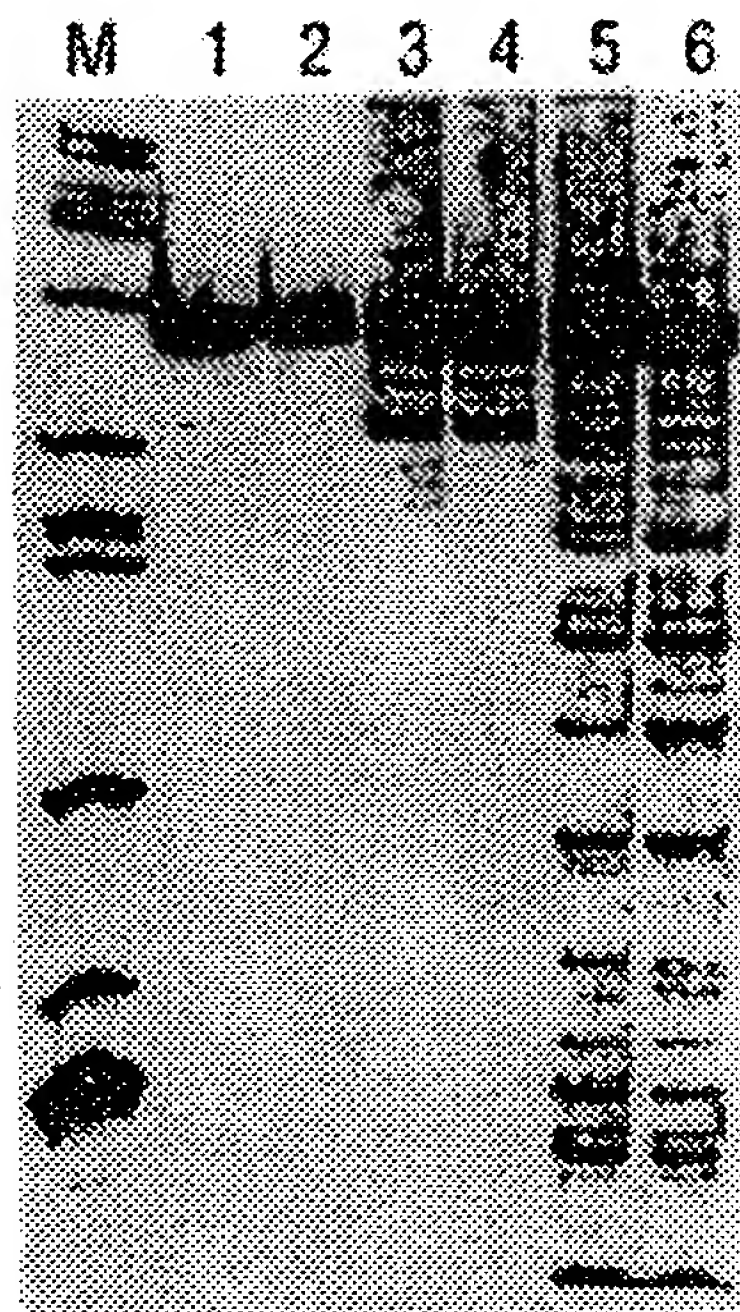


FIG. 30

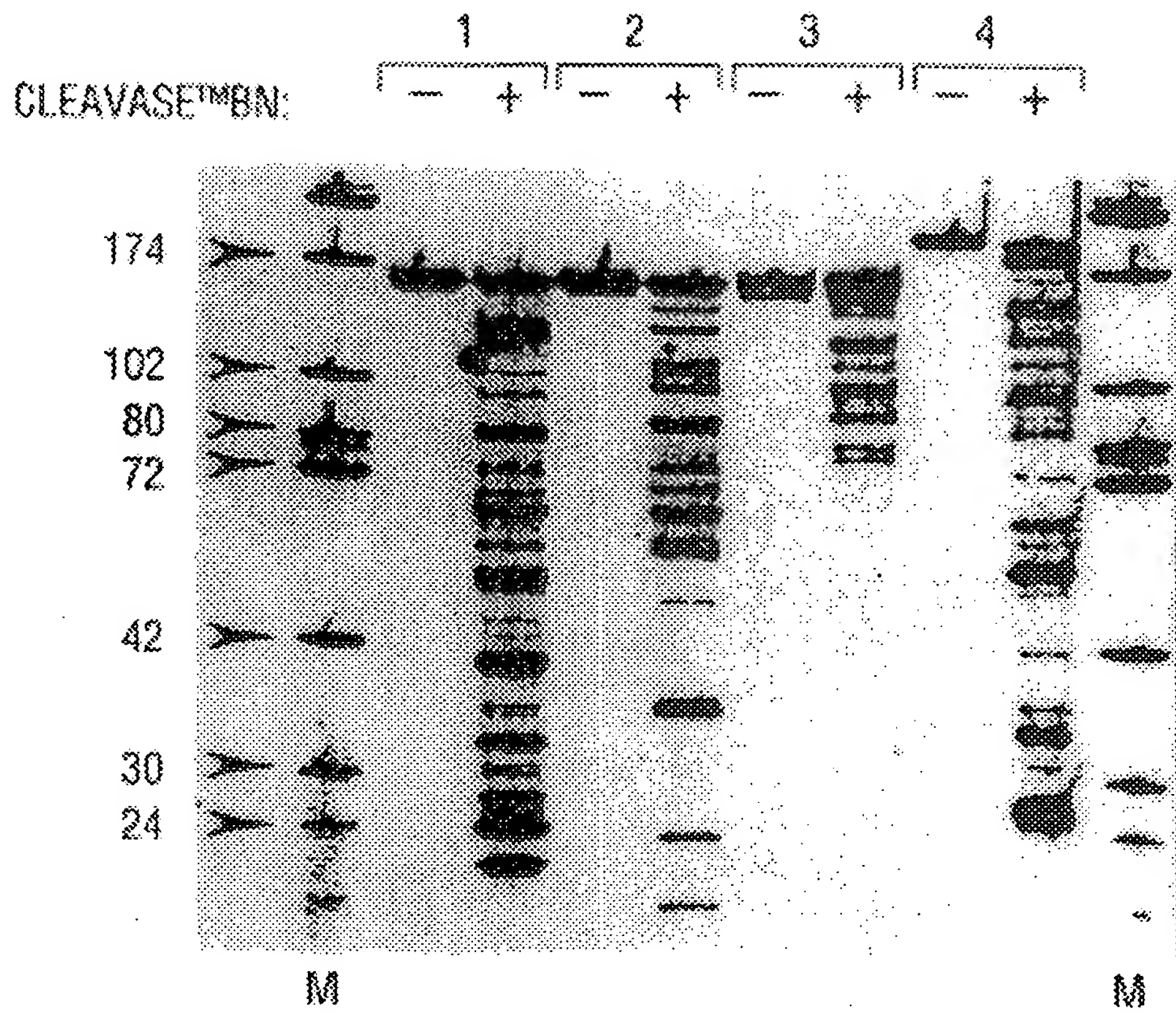


FIG. 31

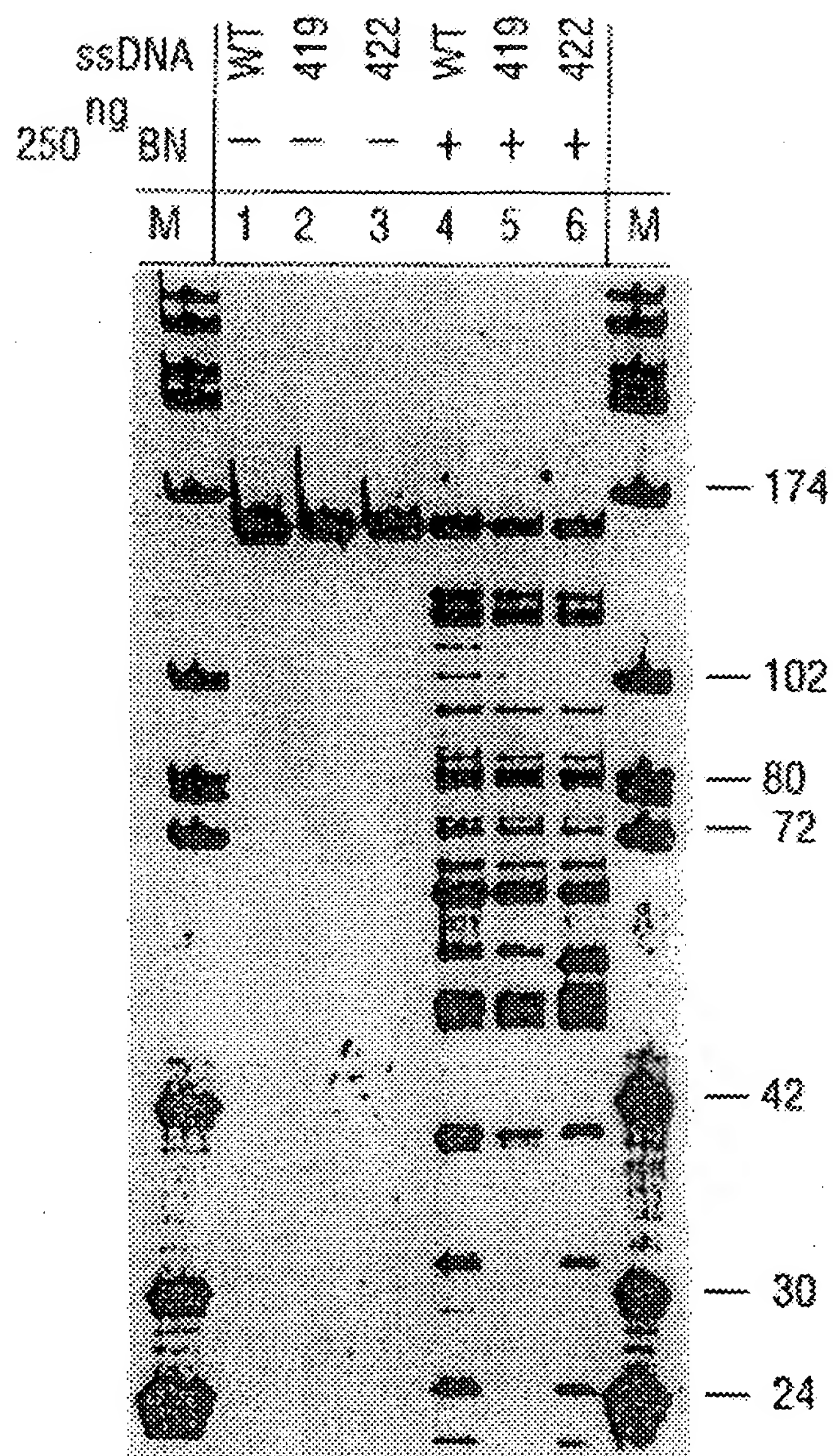


FIG. 32

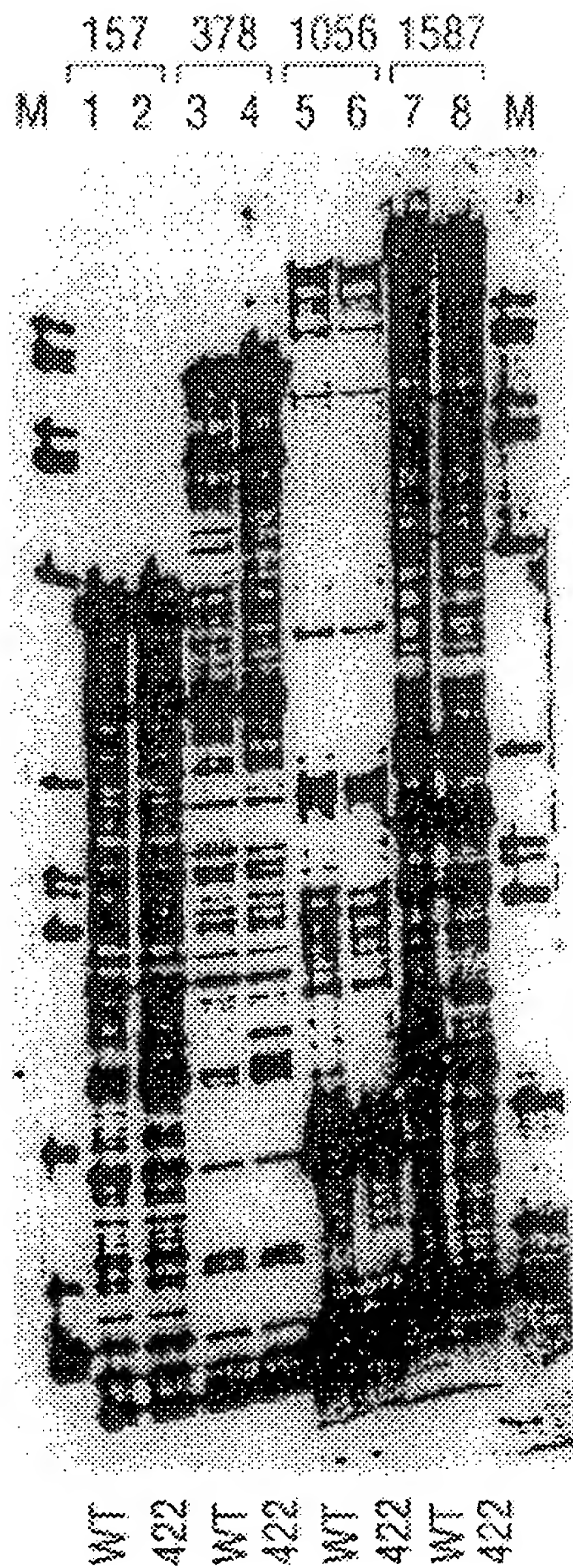


FIG. 33

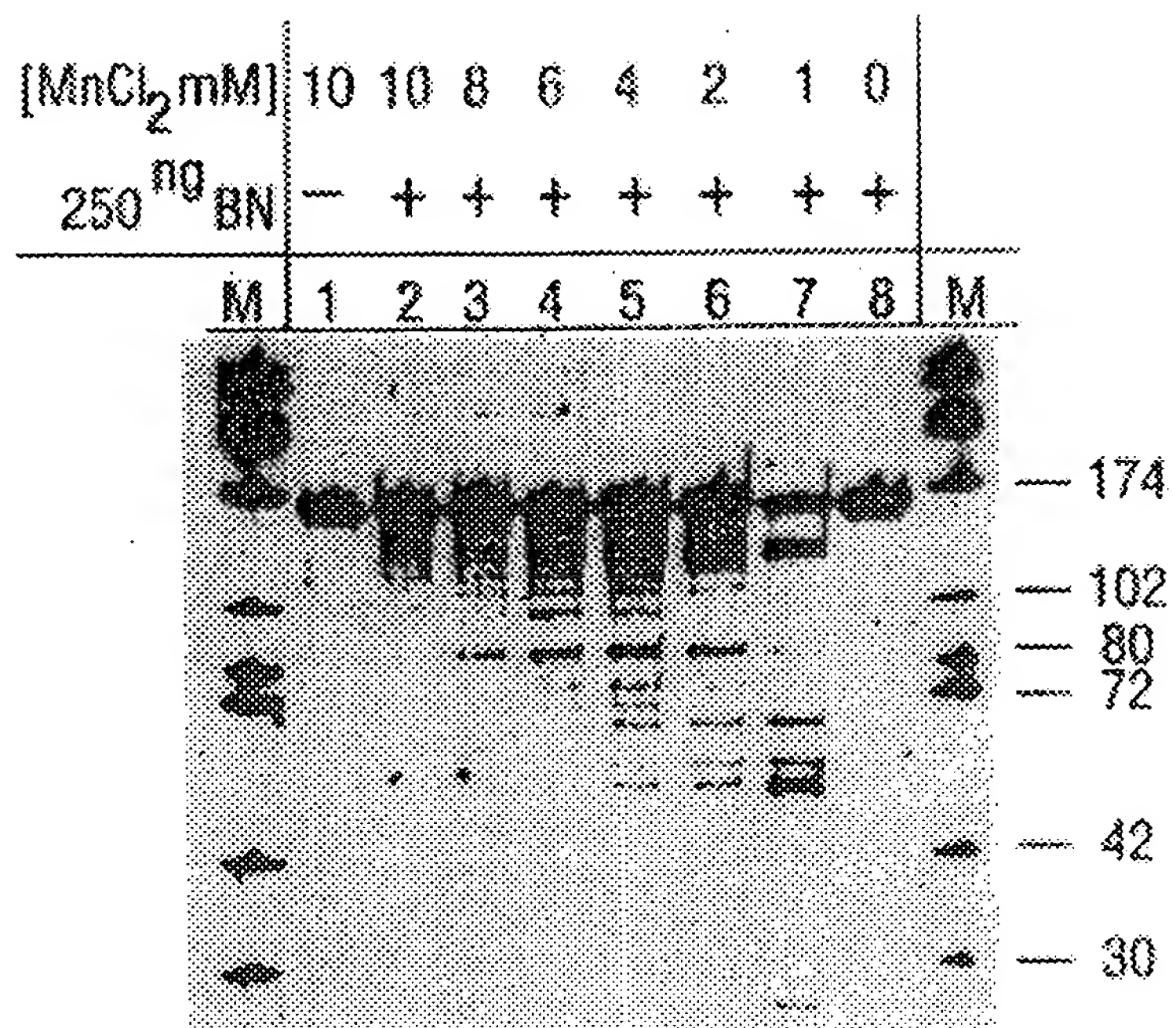


FIG. 34

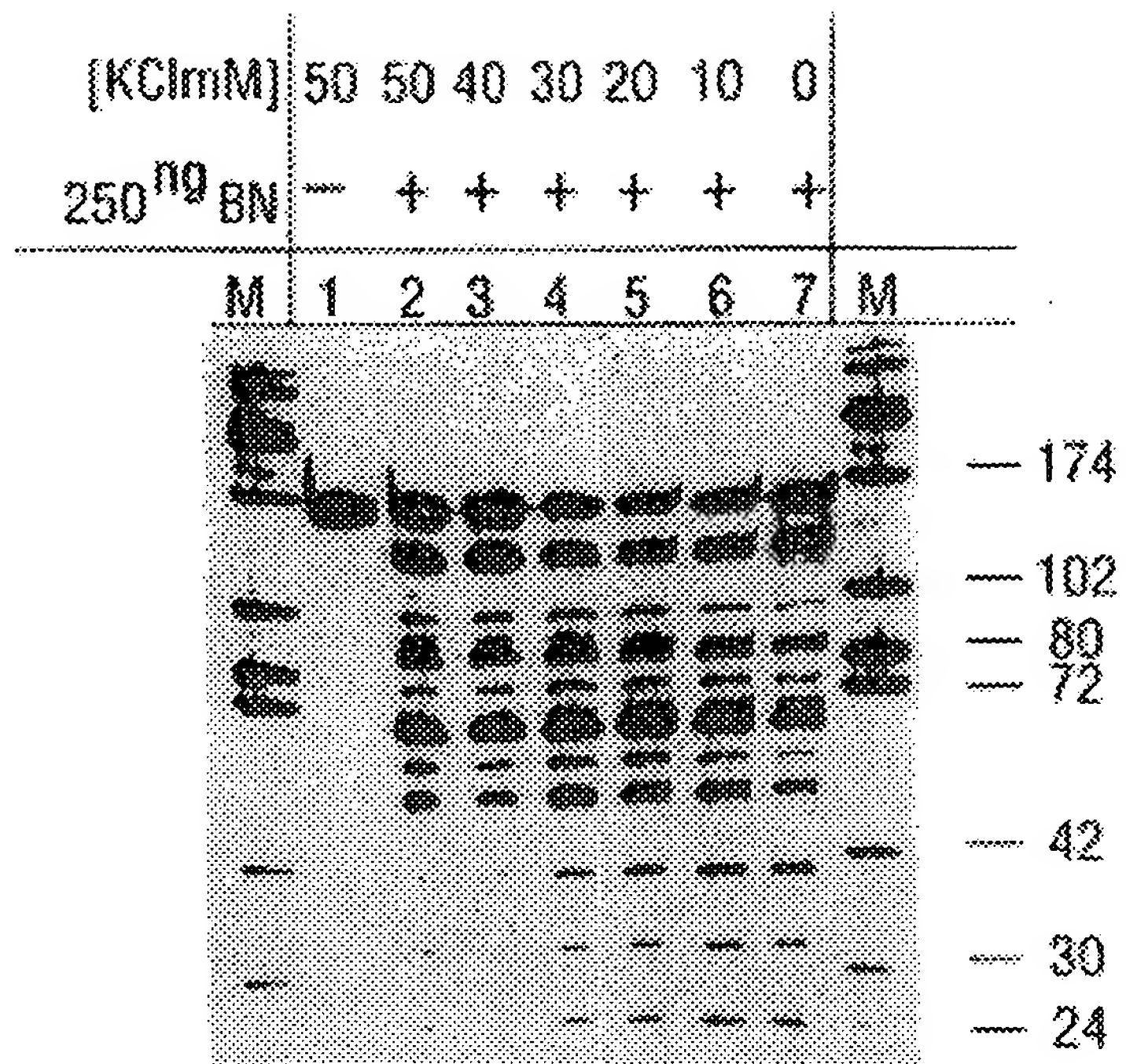


FIG. 35

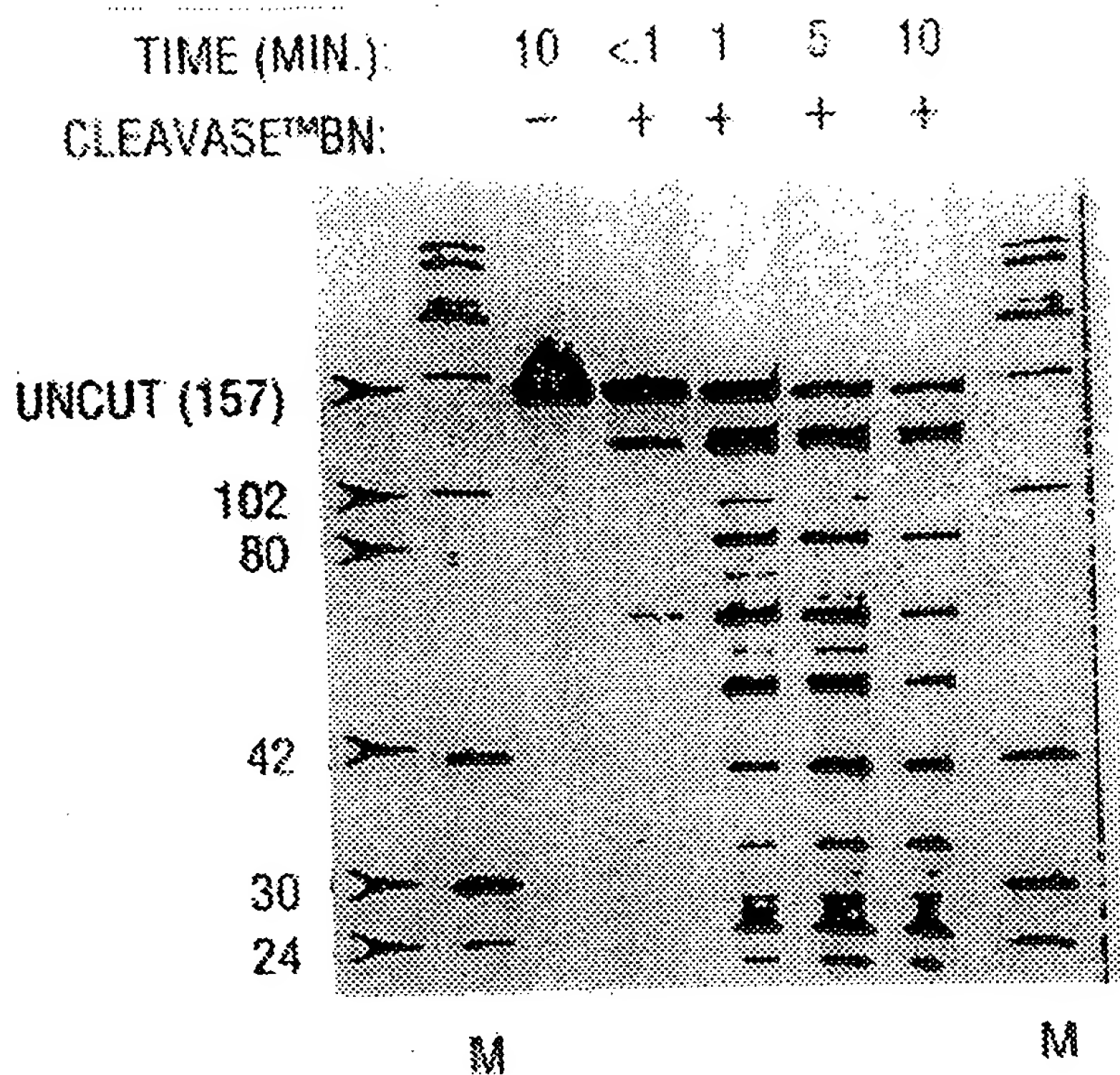


FIG. 36



TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	—	—	+	+	+	+	—	+

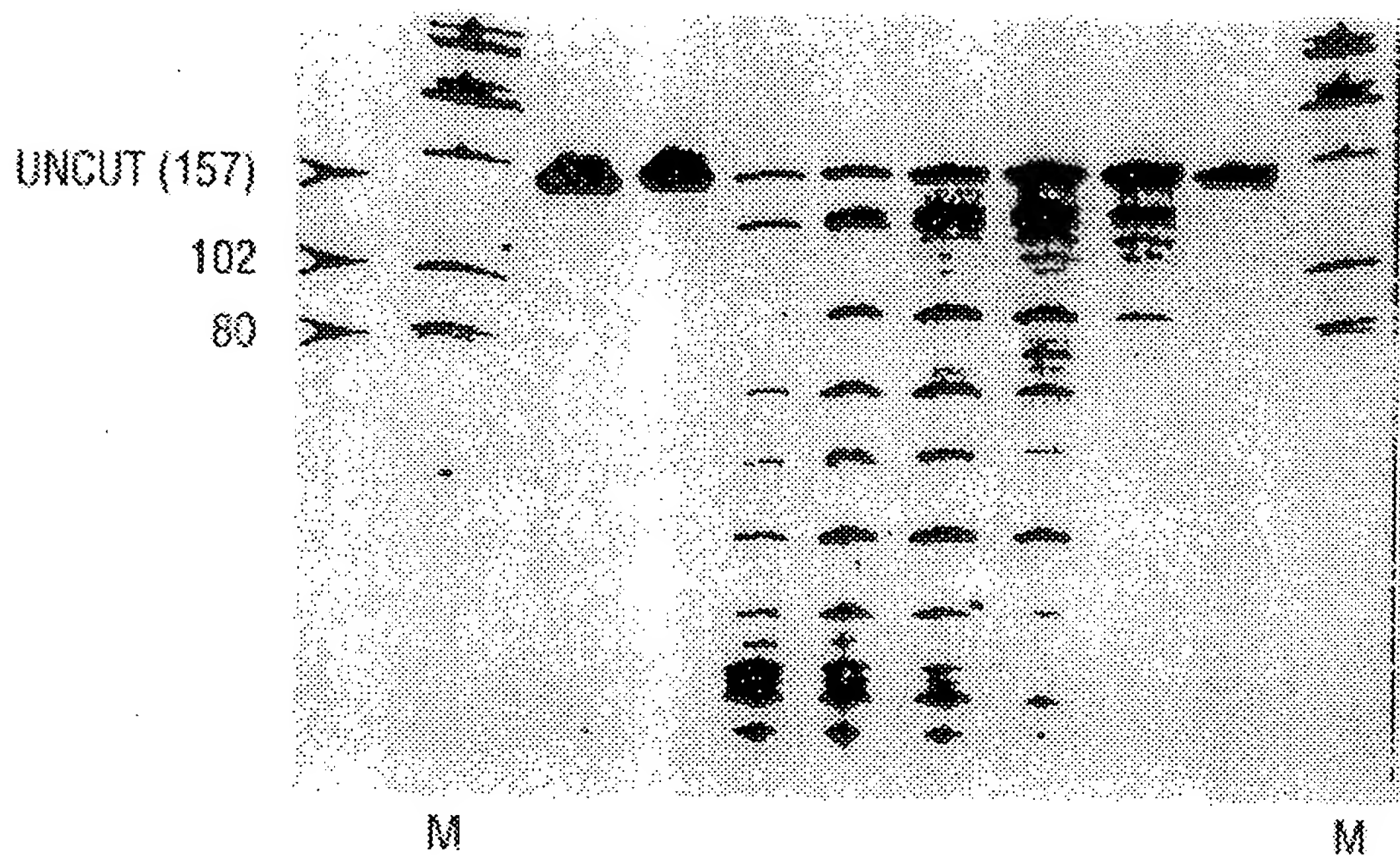


FIG. 37



CLEAVASE™BN (ng): — 10 50 100 250

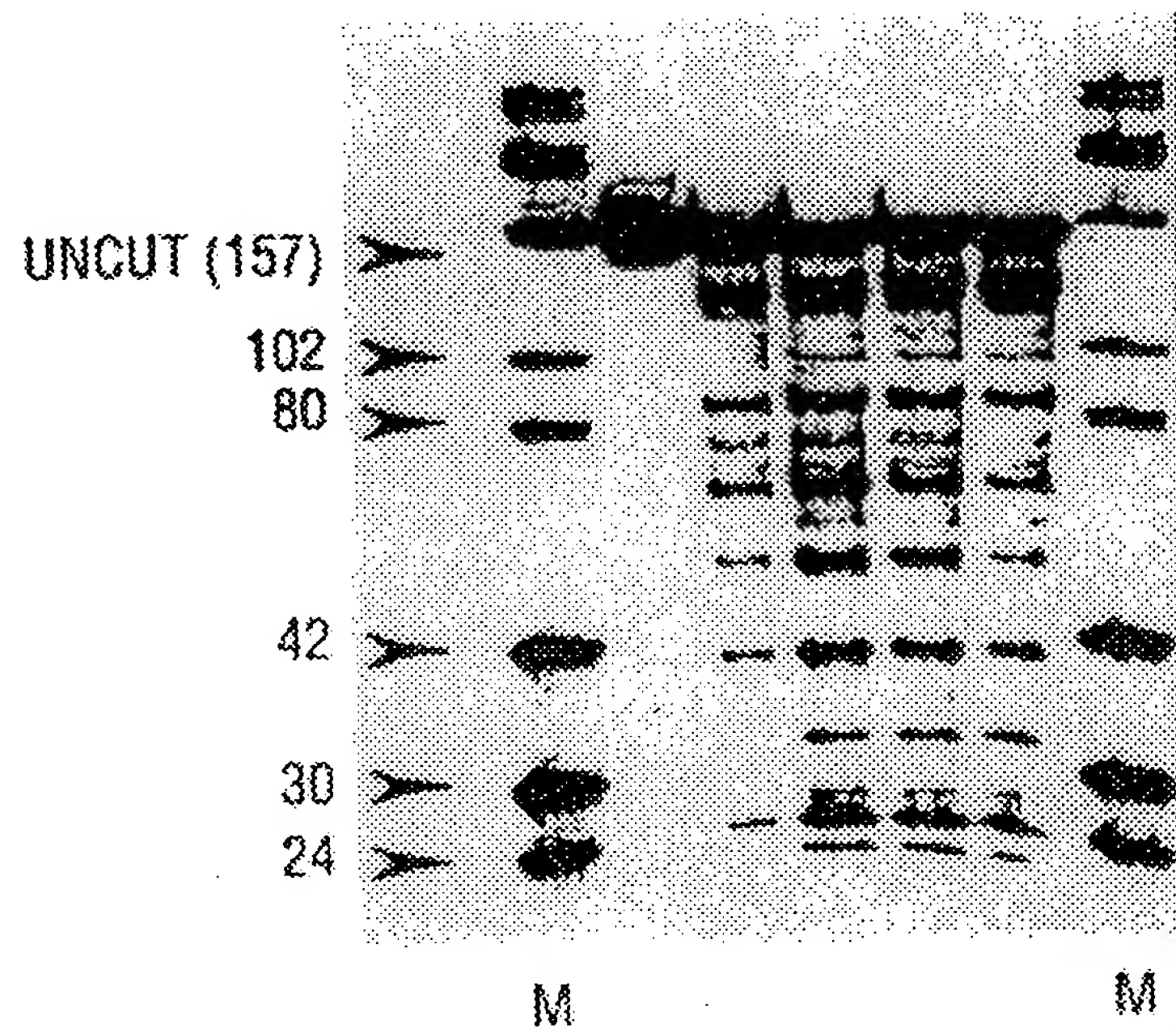


FIG. 38

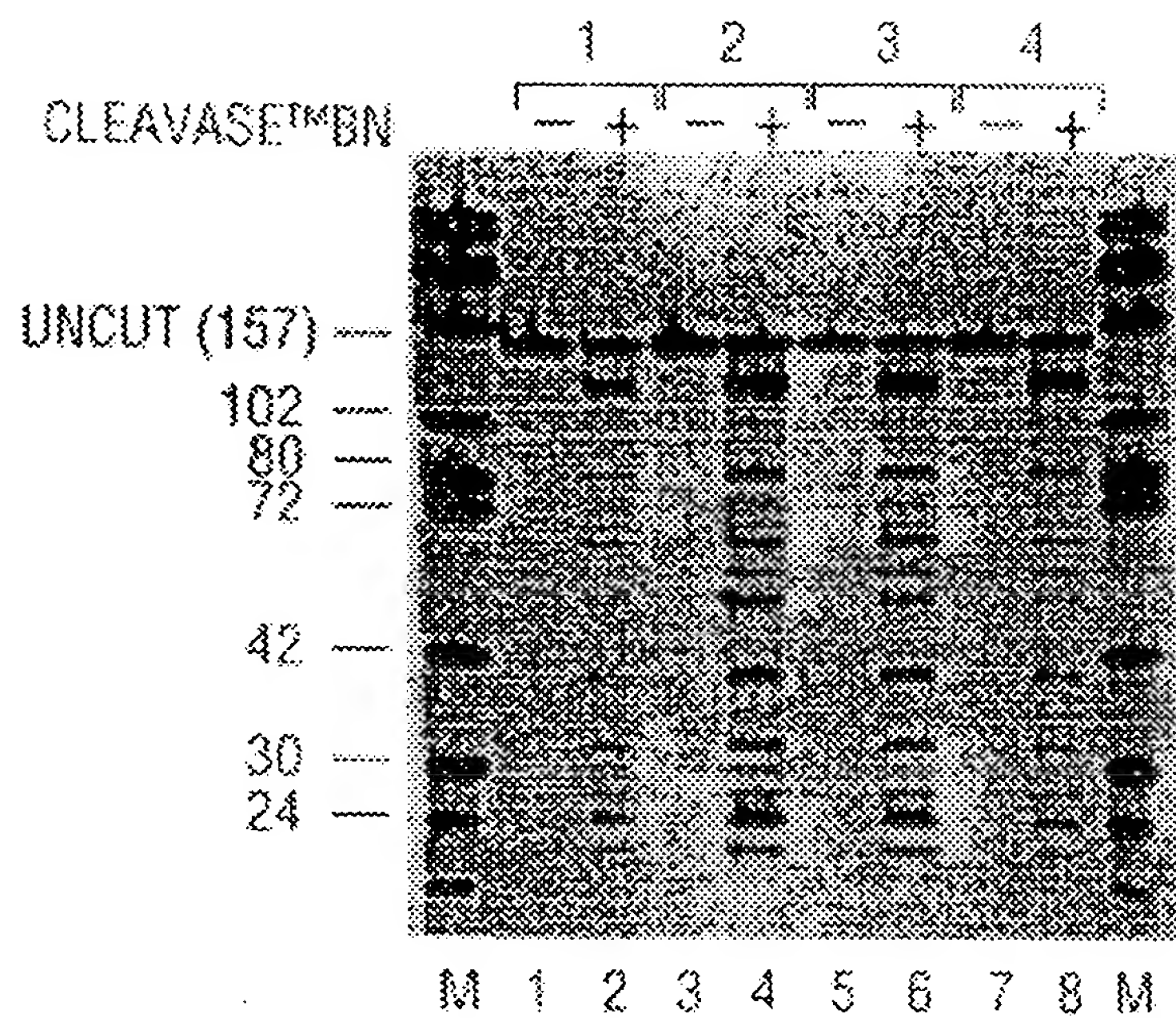


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	—	—	—	—	—	—	—	—	—	—	—	—
250 ^{ng} BN	—	—	—	+	+	+	+	+	+	—	—	—
M	1	2	3	4	5	6	7	8	9	10	11	12

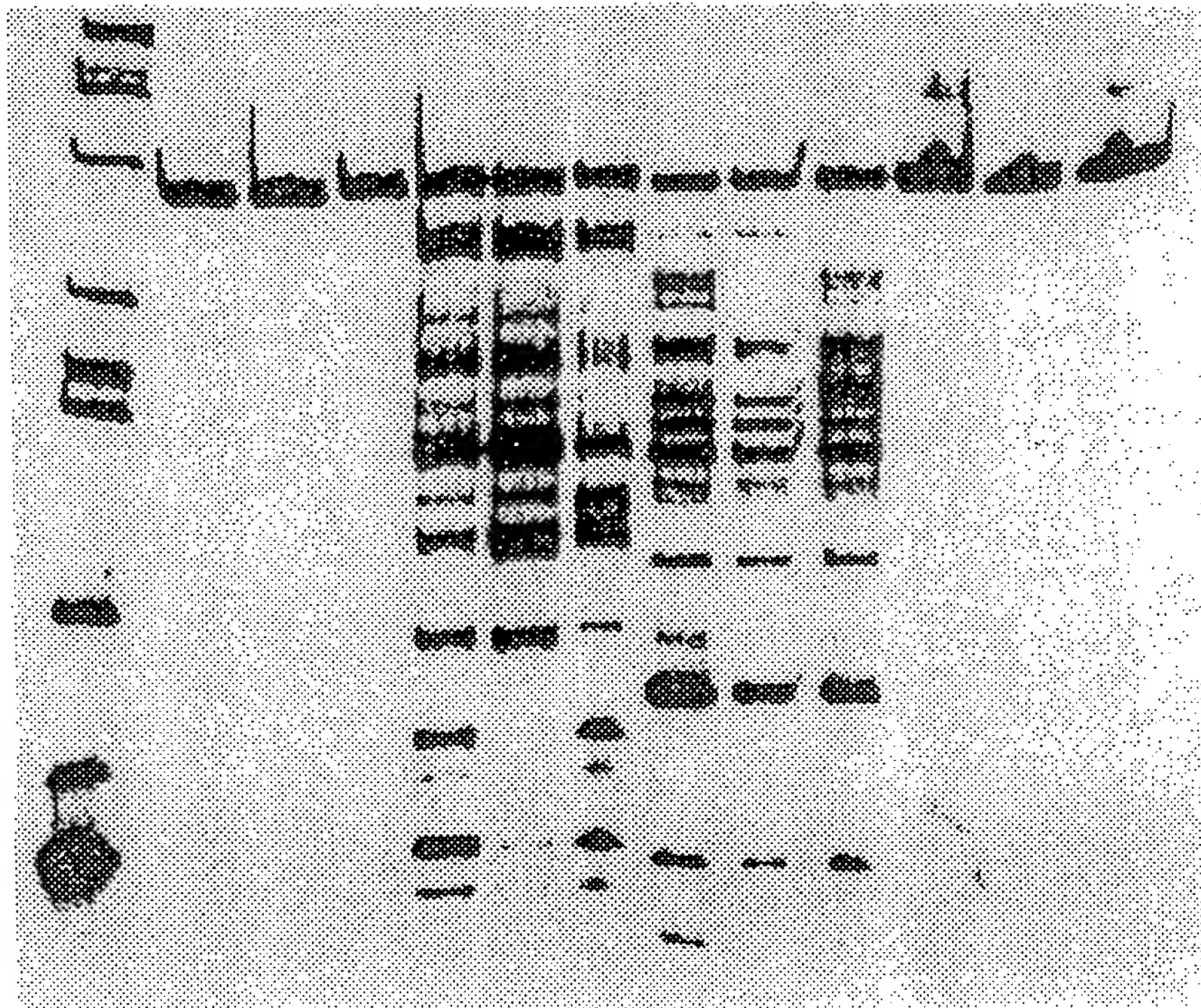


FIG. 40

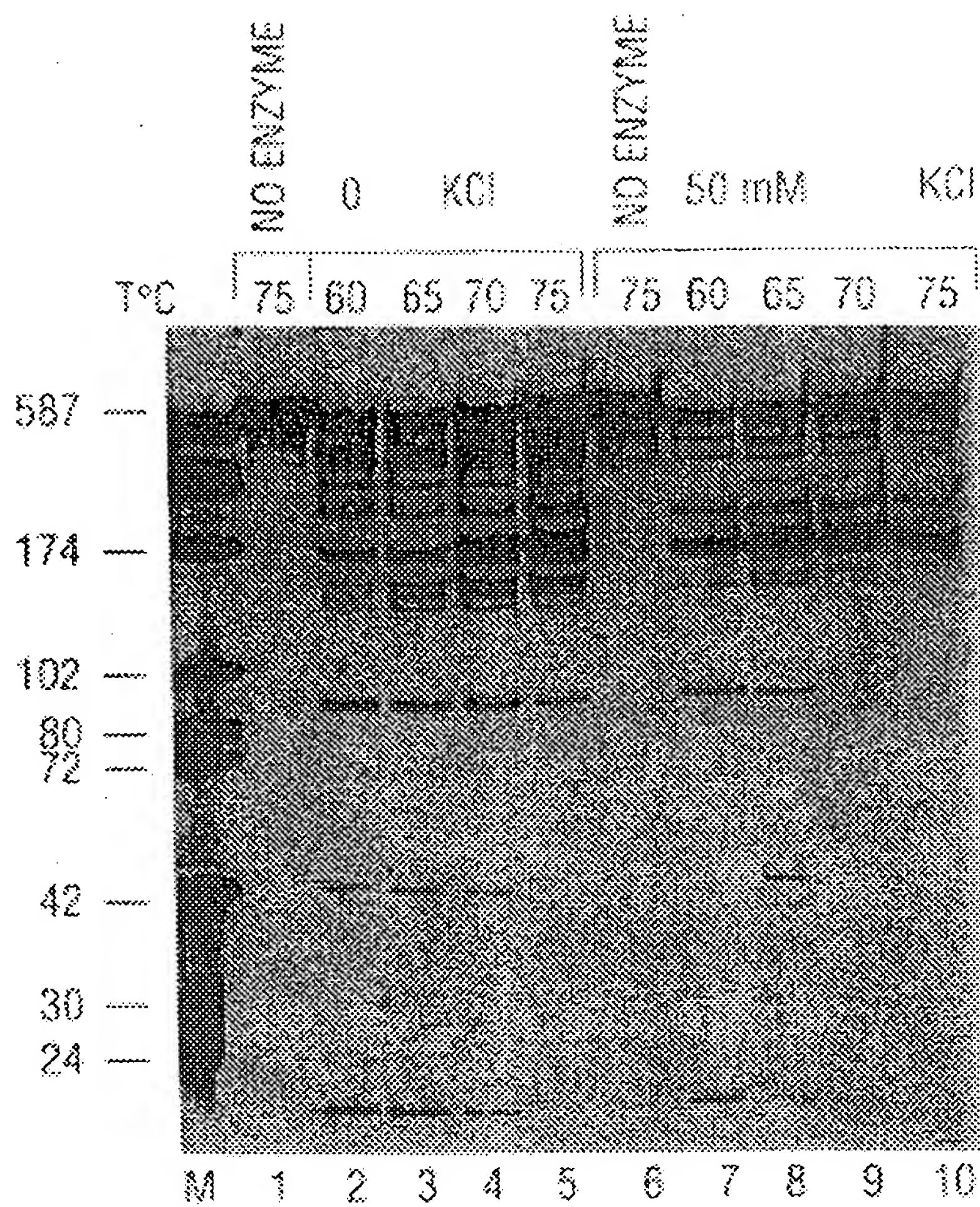


FIG. 41

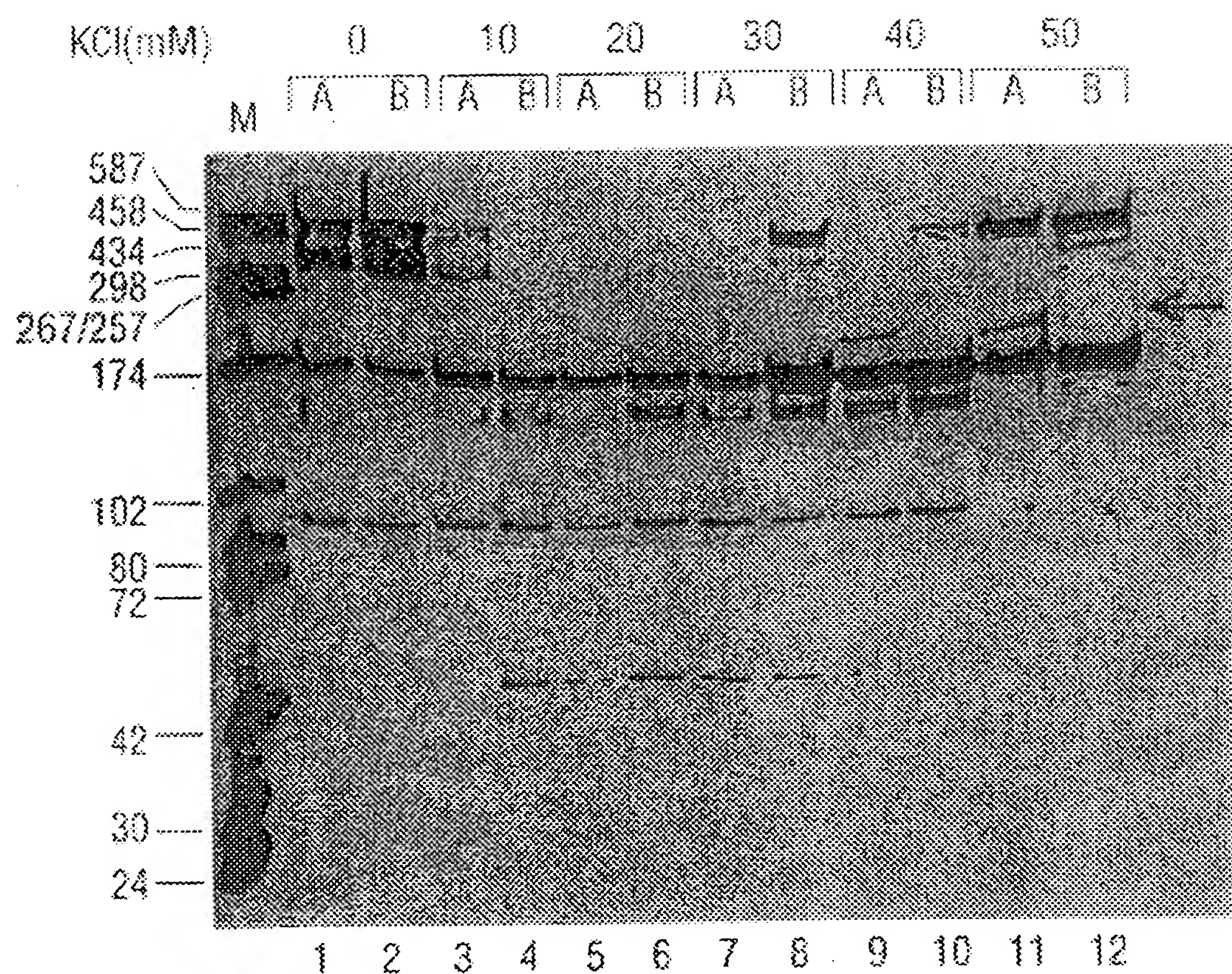


FIG. 42



CLEAVASE™BN

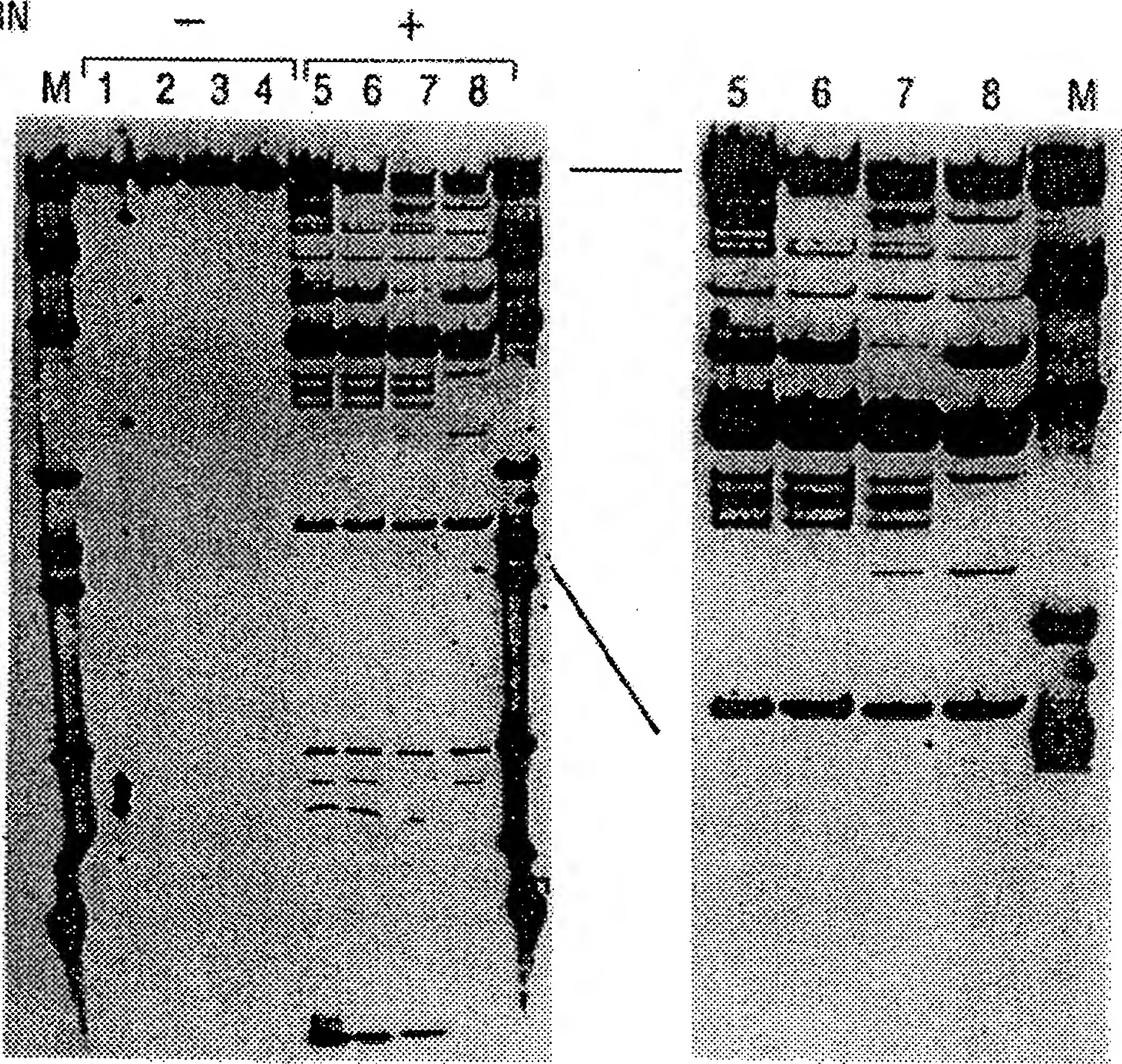


FIG. 43

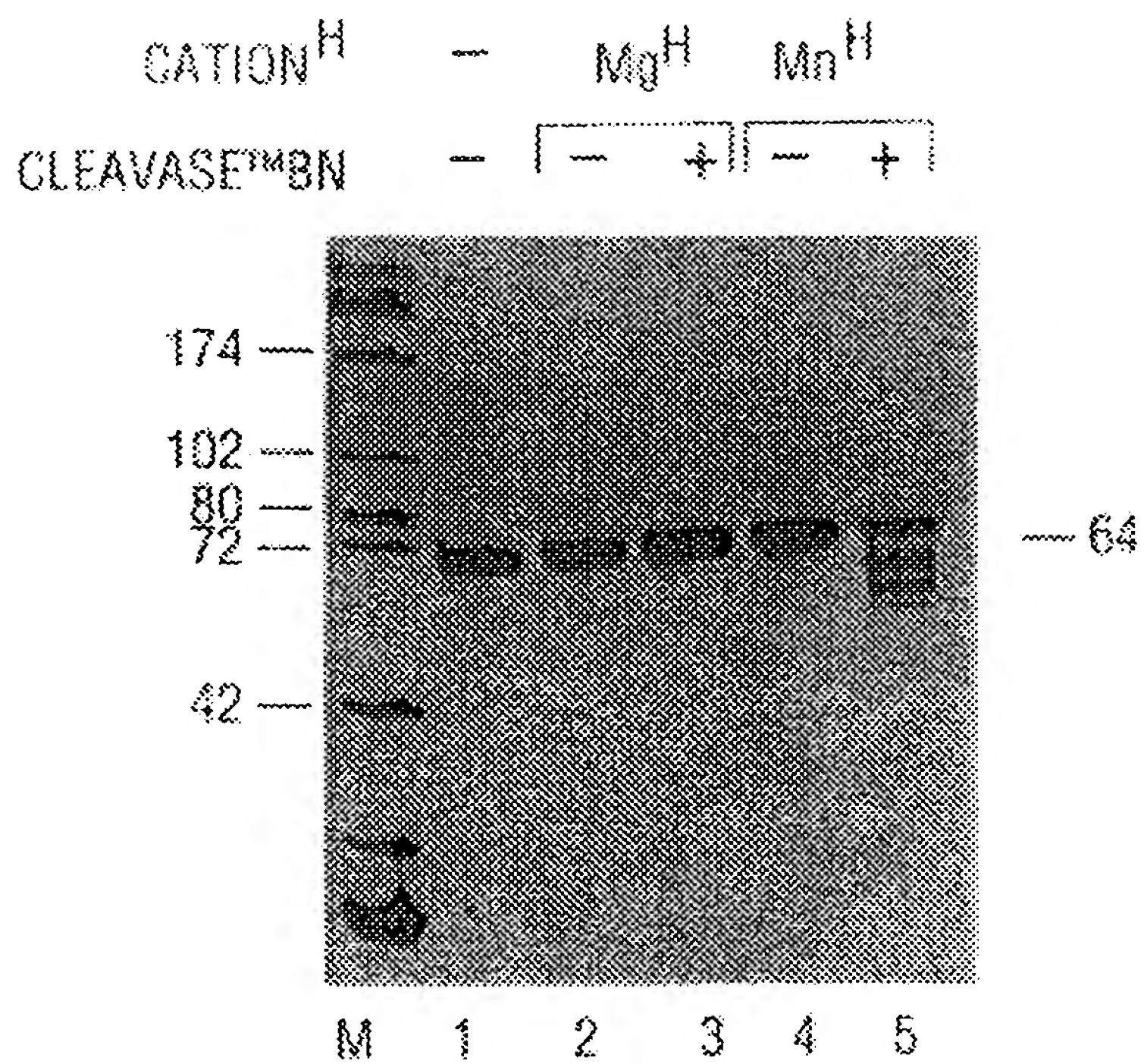


FIG. 44

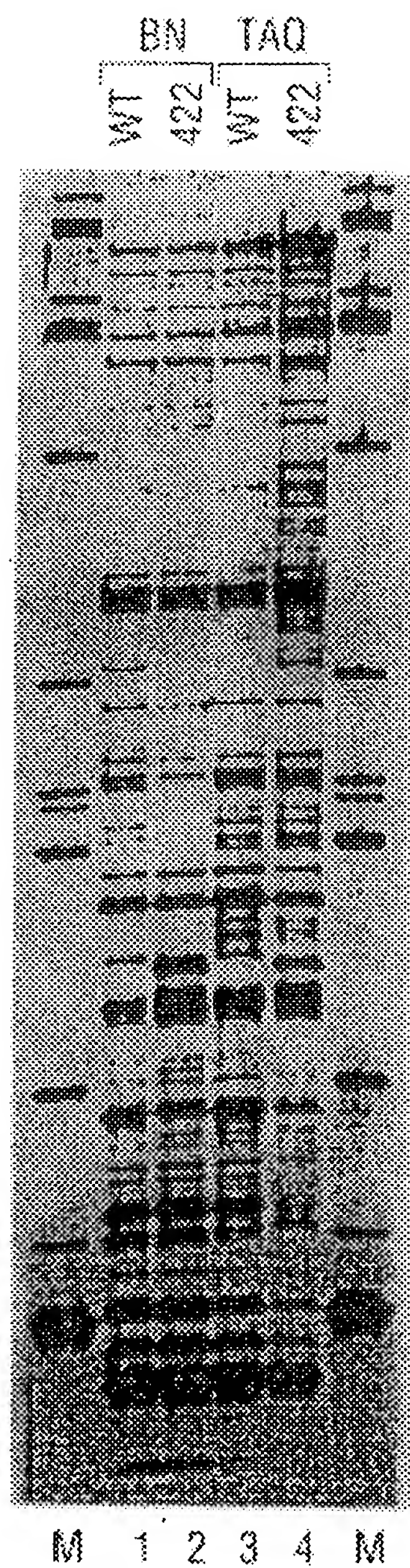


FIG. 45

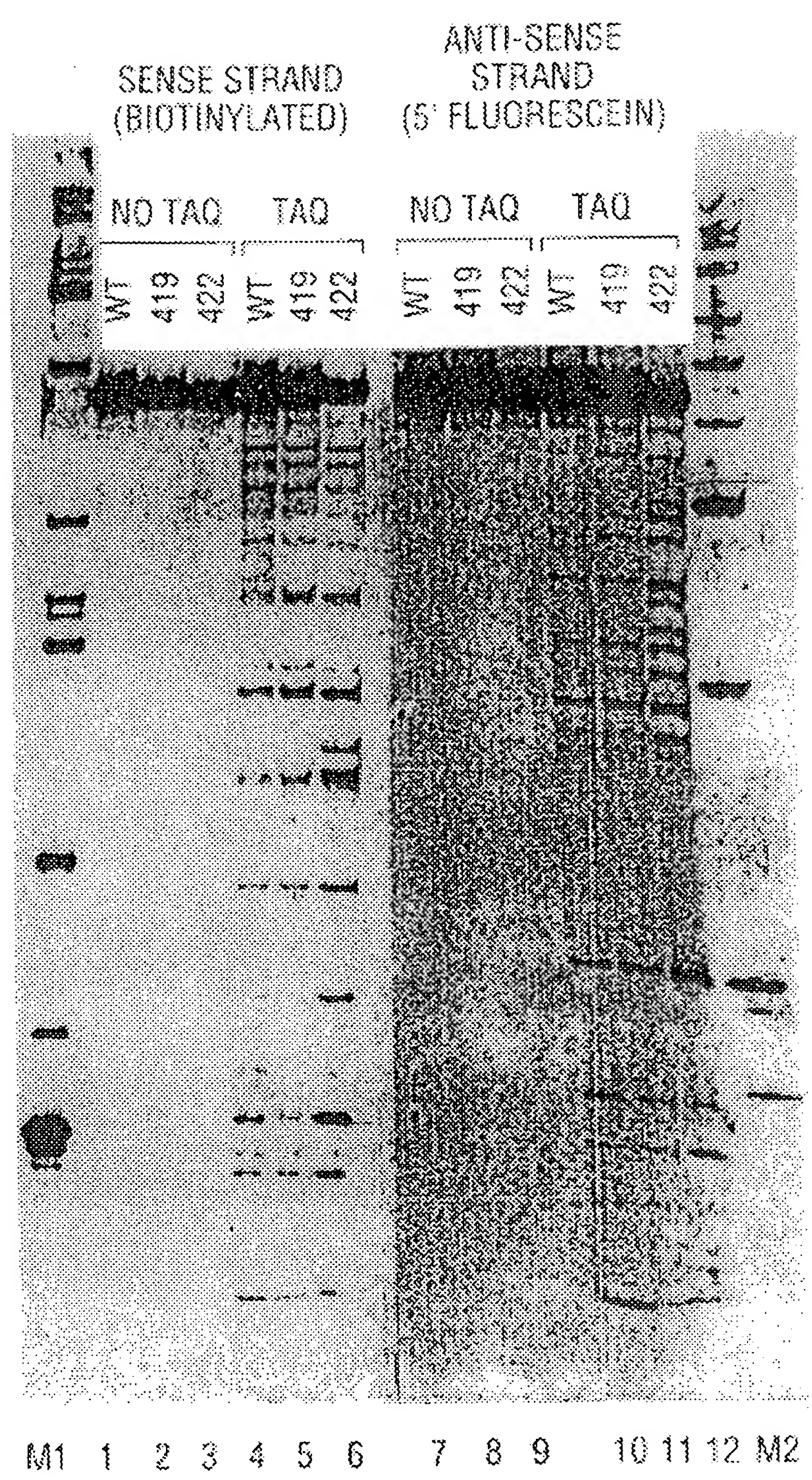
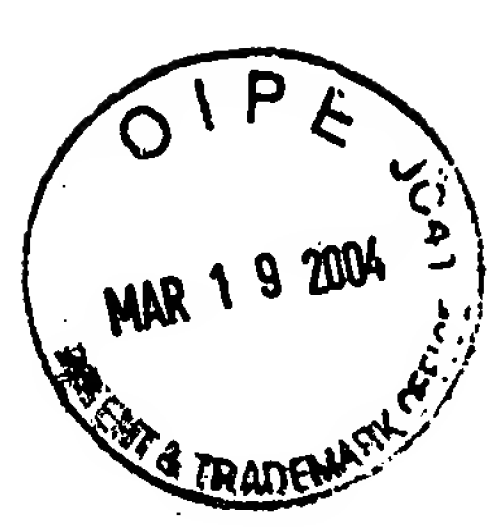


FIG. 46

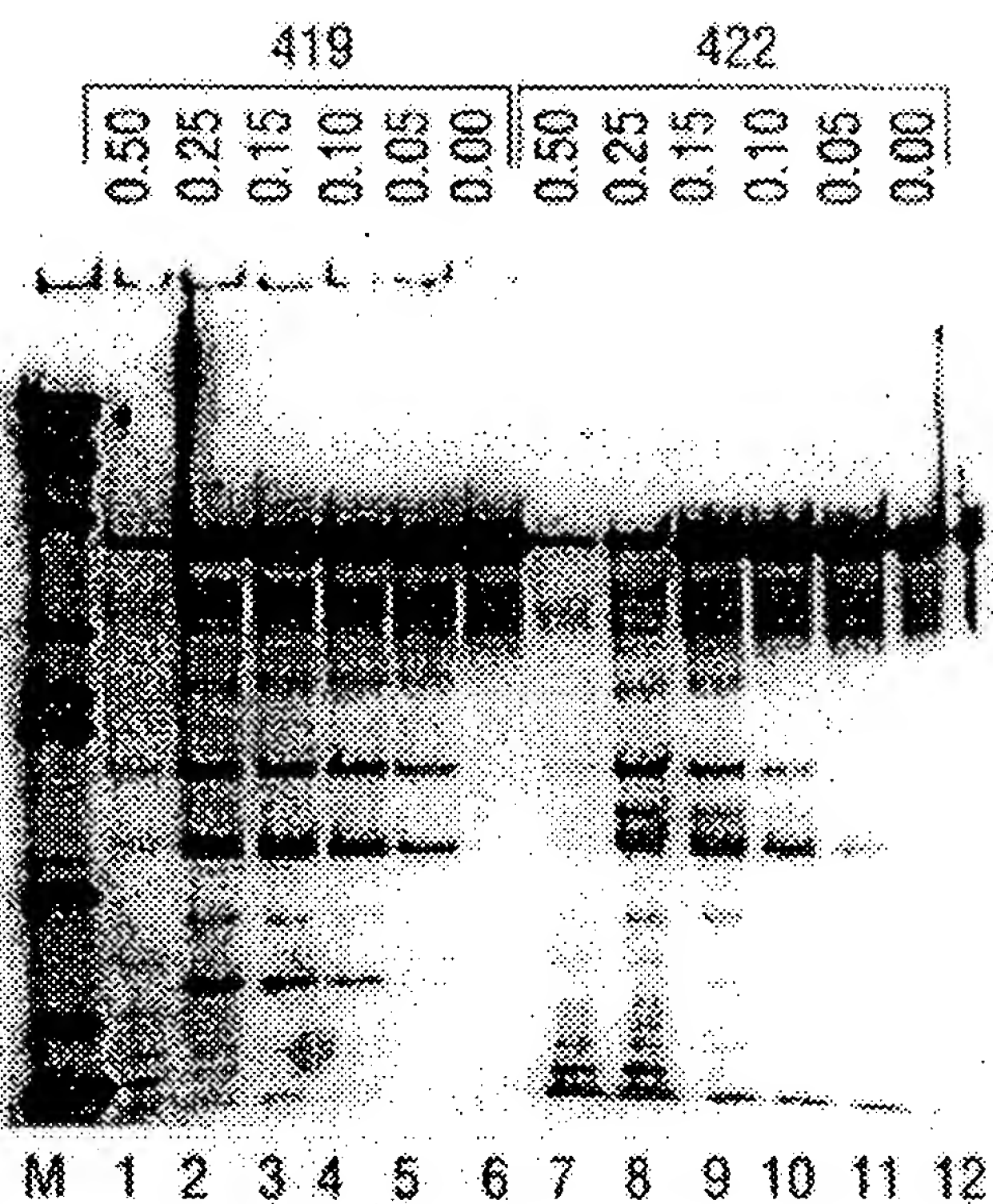


FIG. 47

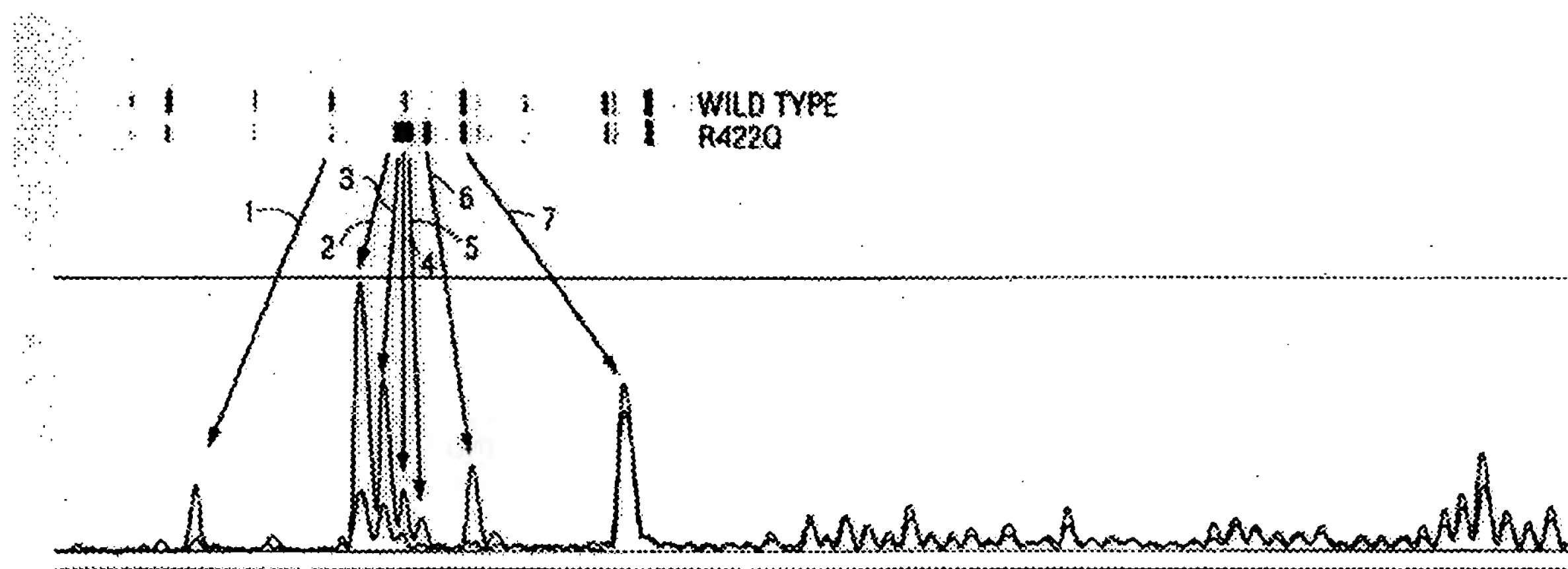


FIG. 48

L.100.8-1 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 76) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 77) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 78) 3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 79) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 80) 3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 81) 3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A



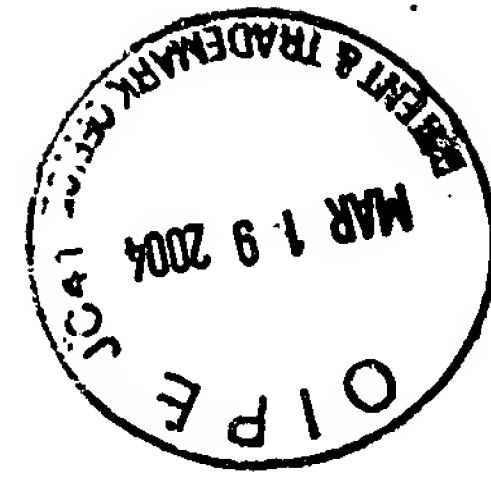
100

L. 100.8-1 (SEQ ID NO: 76)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA
L. 46.16-10 (SEQ ID NO: 77)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA
L. 46.16-12 (SEQ ID NO: 78)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA
L. 19.16-3 (SEQ ID NO: 19)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA
L. CEM/251 (SEQ ID NO: 80)	ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCTTTCT TACAATGCCCCCTCCATGACCCCTTCCTCGGCCAGCCCTTGCGGGTGAAAGA
L. 36.8-3 (SEQ ID NO: 81)	ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA

FIG. 49B

L.100.8-1	5'TGATGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.46.16-10	5'TGATGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.46.16-12	5'TGGTGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACCACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.19.16-3	5'TGATGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.CEM/251	5'TGATGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.36.8-3	5'TGATGTATAAATATCACTGCAATTTTCGCTCTGTATTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT

FIG. 49C



L. 100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCAAGAGAGGTCGTGATCGTCCATC	200
L. 46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCAAGAGAGGTCGTGATCGTCCATC	
L. 46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCAAGAGAGGTCGTGATCGTCCATC	
L. 19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCAAGAGAGGTCGTGATCGTCCATC	
L. CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCAAGAGAGGTCGTGATCGTCCATC	
L. 36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D





L. 100. 8 -1	5' AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCACTTGGCCGGTGCTGGG	250
(SEQ ID NO: 76)	3' TCGGACCCACAAGGGACCATCTG	AGAGTGGTCGTGAACCGGCCACGACCC	
L. 46.16-10	5' AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCACTTAGCCAGTGCTGGG	
(SEQ ID NO: 77)	3' TCGGACCCACAAGGGACGATCTG	AGAGTGGTCGTGAATCGGTCACGACCC	
L. 46.16-12	5' AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCACTTGGCCAGTGCTGGG	
(SEQ ID NO: 78)	3' TCGGACCCACAAGGGACGATCTG	AGAGTGGTCGTGAACCGGTCACGACCC	
L. 19.16-3	5' AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCACTTGGCCGGTGCTGGG	
(SEQ ID NO: 79)	3' TCGGACCCACAAGGGACGATCTG	AGAGTGGTCGTGAACCGGCCACGACCC	
L. CEM/251	5' AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGCACTTGGCCGGTGCTGGG	
(SEQ ID NO: 80)	3' TCGGACCCACAAGGGACGATCTG	AGAGTGGTCGTGAACCGGCCACGACCC	
L. 36.8-3	5' AGCCTGAGTGTTCCCTGCTAAAC	TCTCACCAGCACTTGGCCGGTGCTGGG	
(SEQ ID NO: 81)	3' TCGGACTCACAAAGGGACGATTTG	AGAGTGGTCGTGAACCGGCCACGACCC	
			HAIRPIN

FIG. 49E



350

L. 100. 8-1	5' ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATCCGGTCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'
L. 46, 16-10	5' ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATTCGGTCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'
L. 46. 16-12	5' ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATTCGGTCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'
L. 19, 16-3	5' ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATCCGATCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'
L. CEM/251	5' ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATTCGATCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'
L. 36. 8-3	5' ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG	G 3'
	3' TAAATCTTTCATCCGATCACACACACAGGGTAGAGAGGATCGGCGCGGAC	C 5'

FIG. 49G

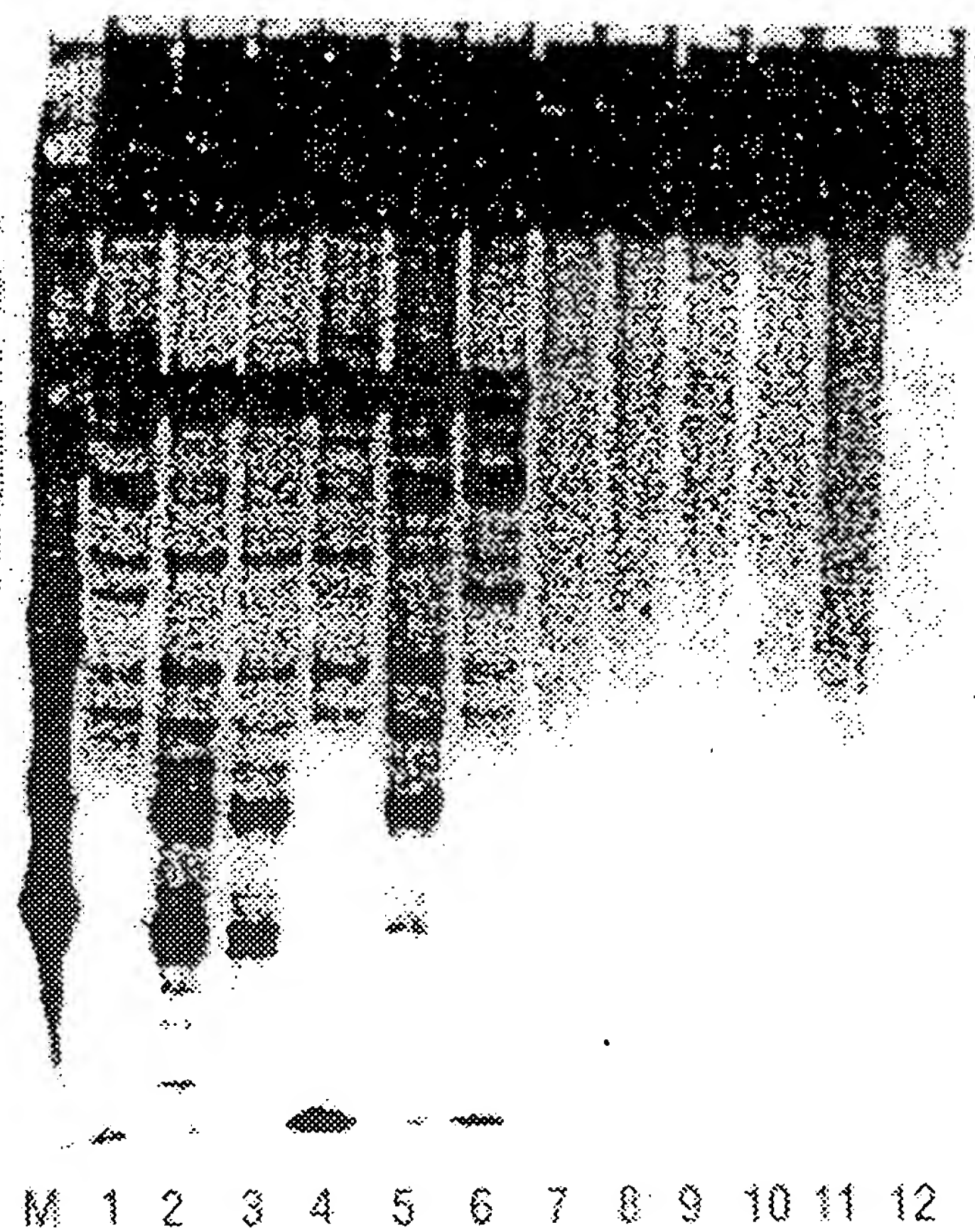


FIG. 50

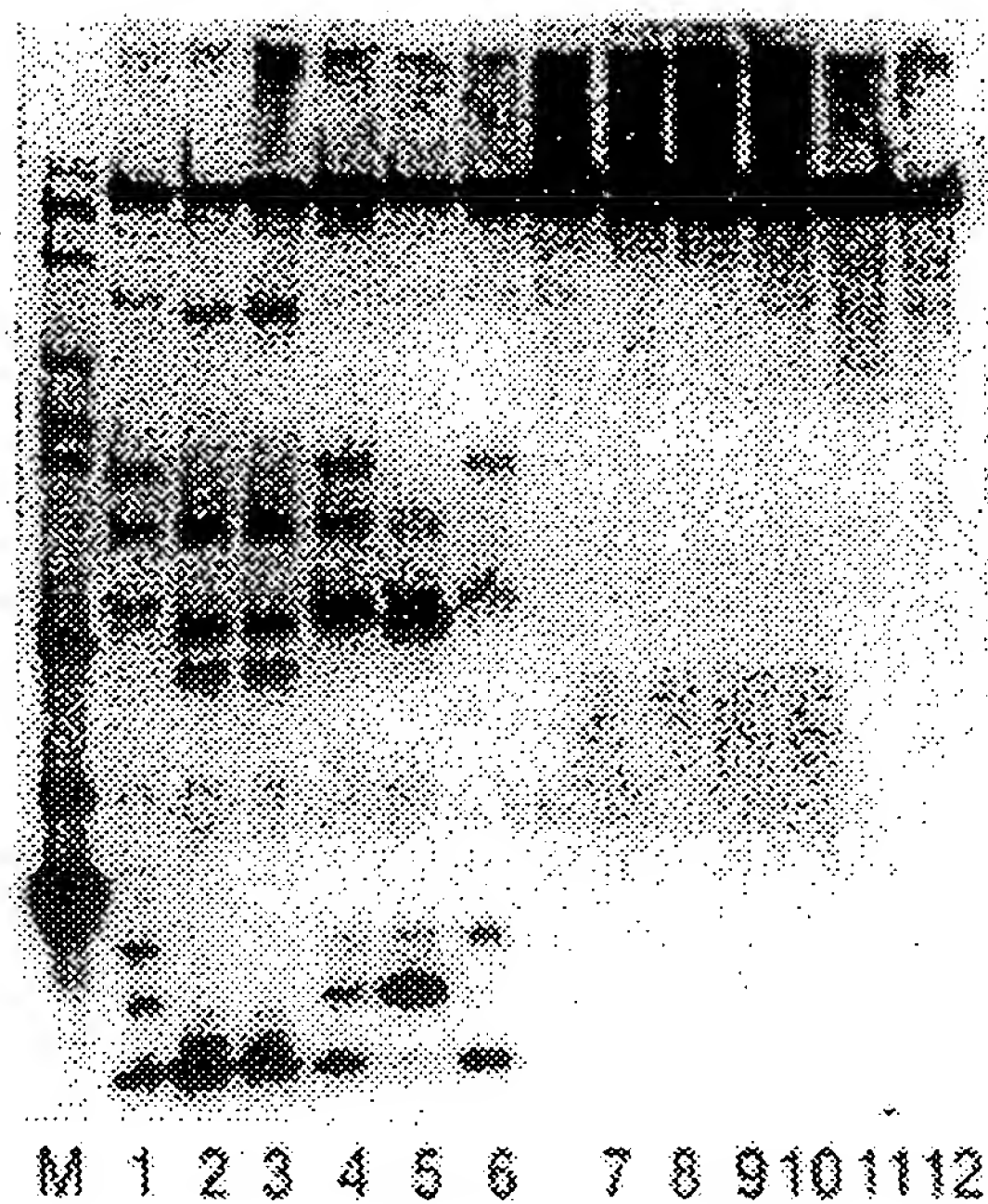


FIG. 51

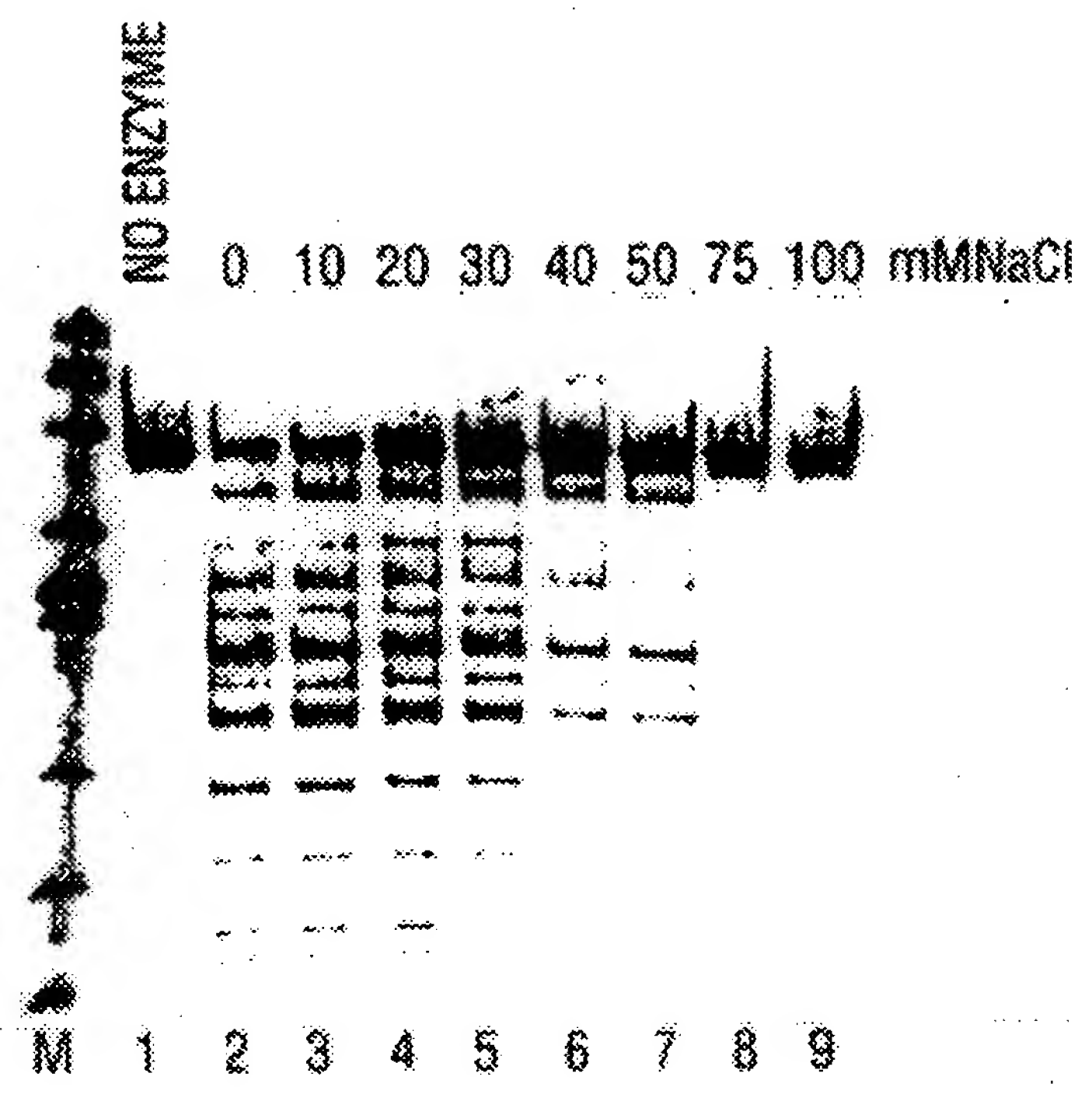


FIG. 52

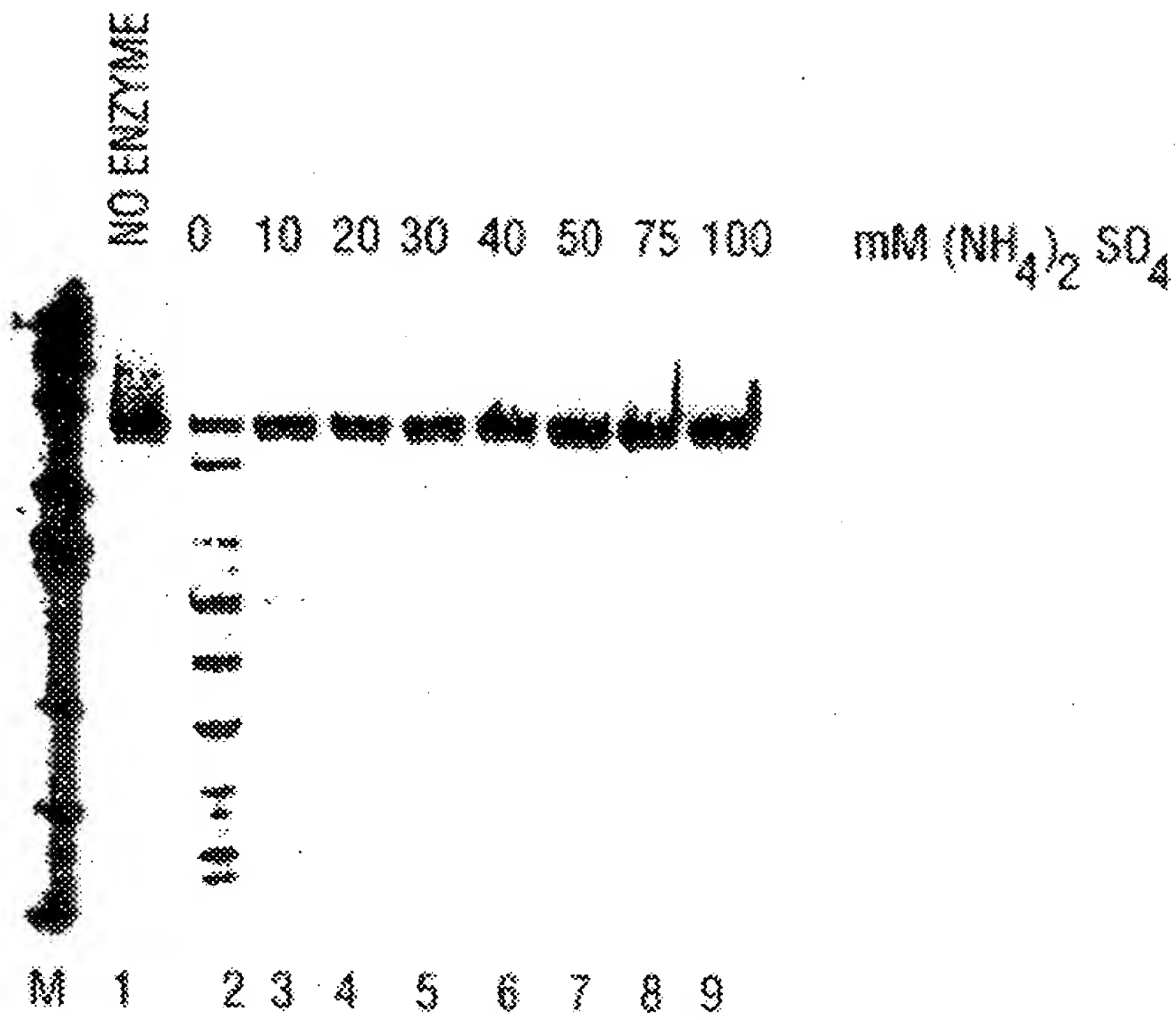


FIG. 53

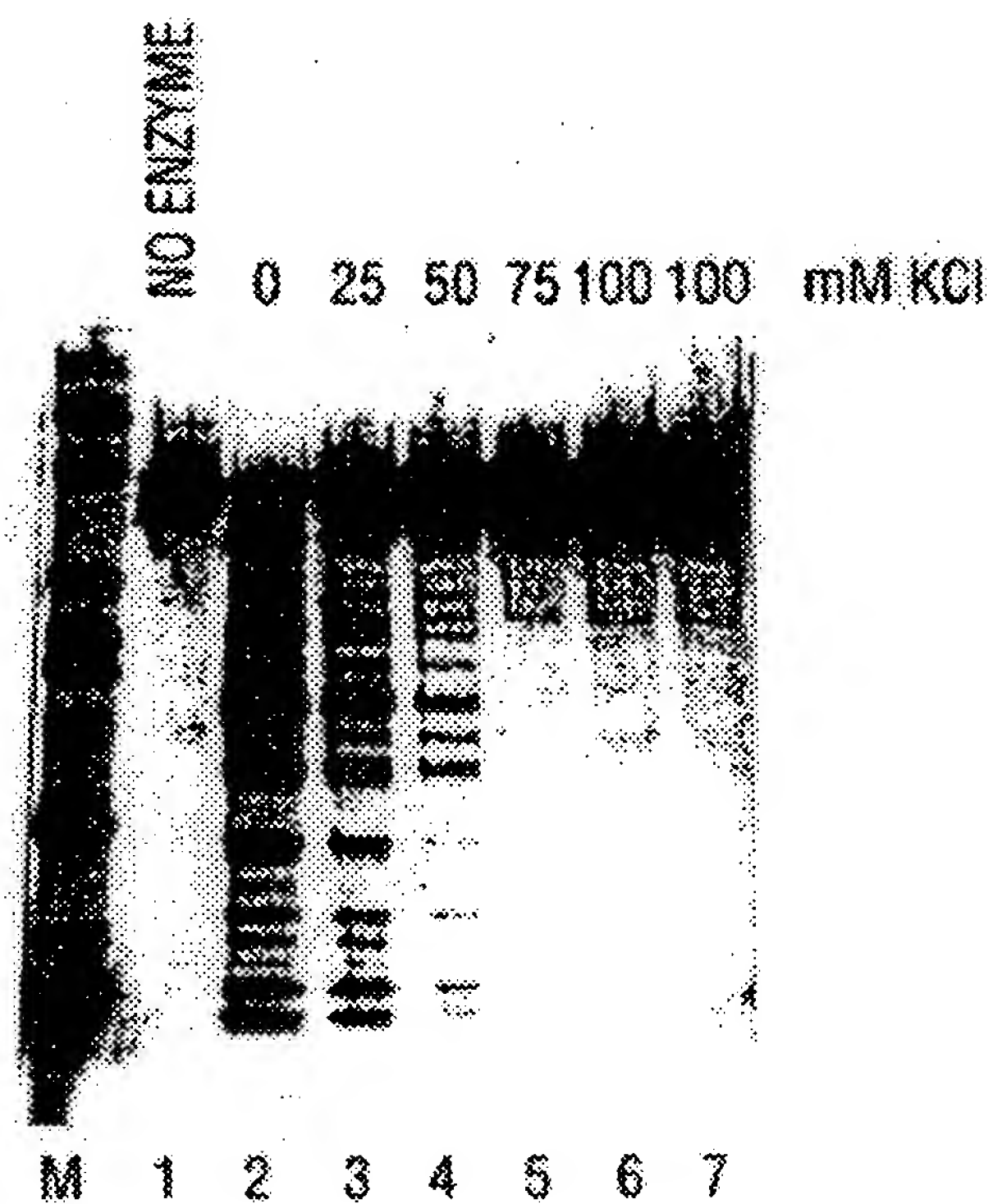


FIG. 54

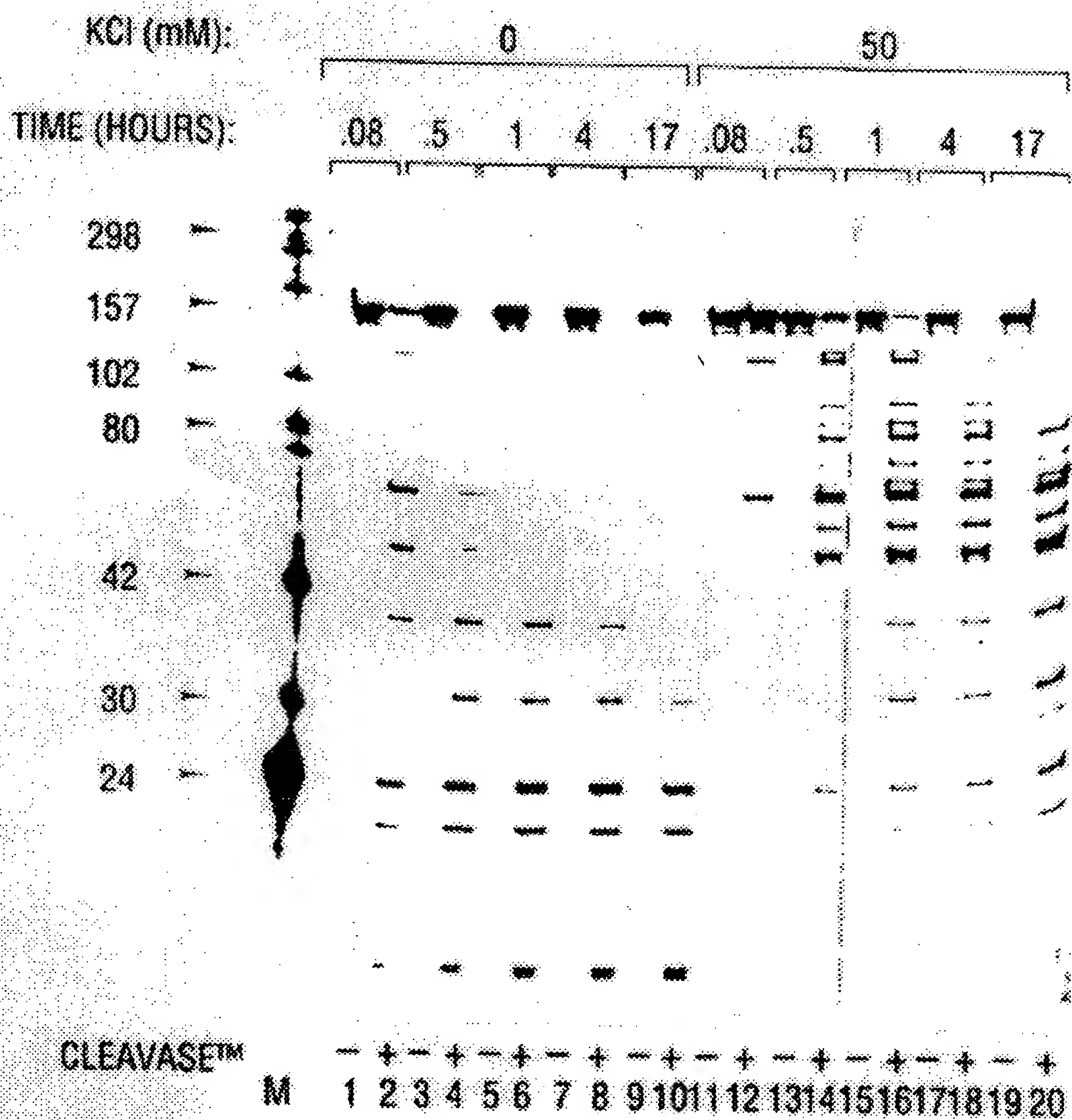


FIG. 55

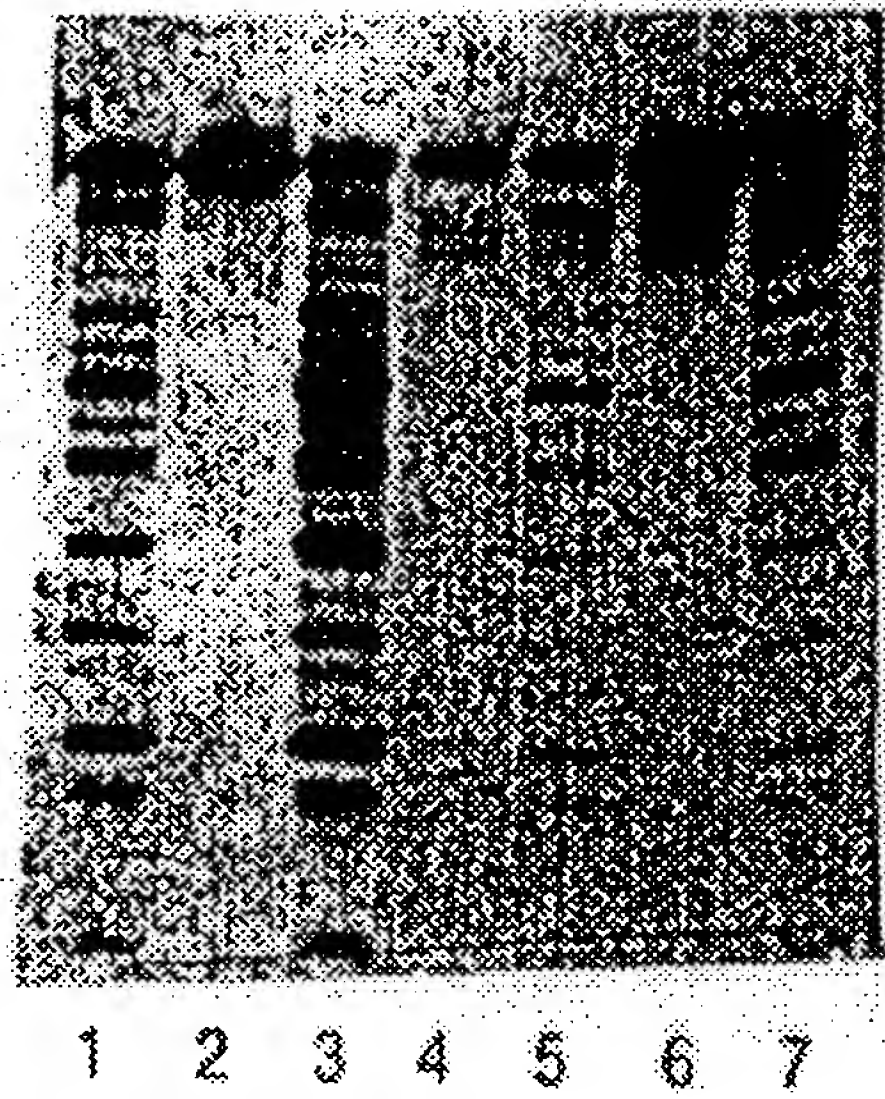


FIG. 56

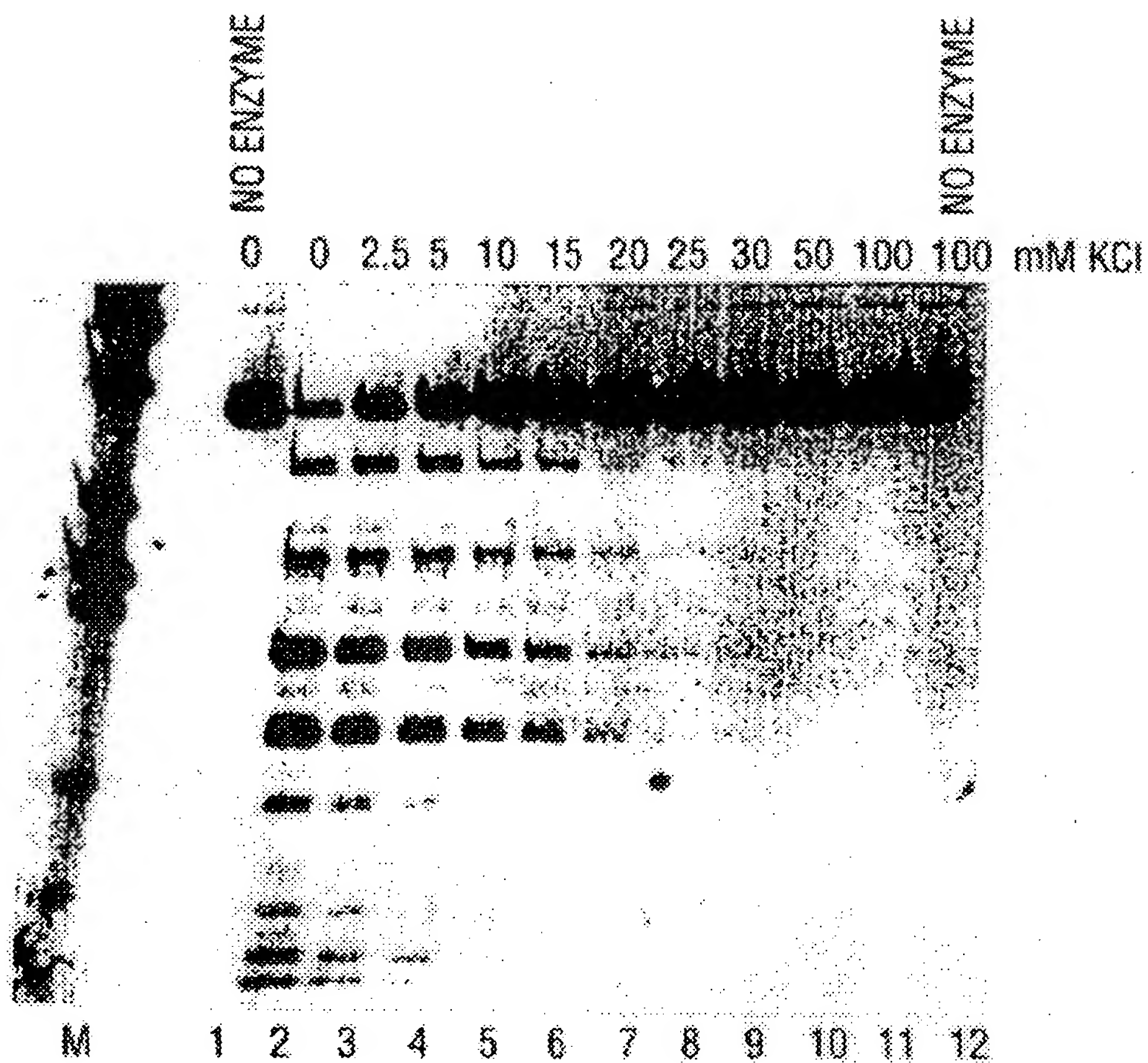


FIG. 57

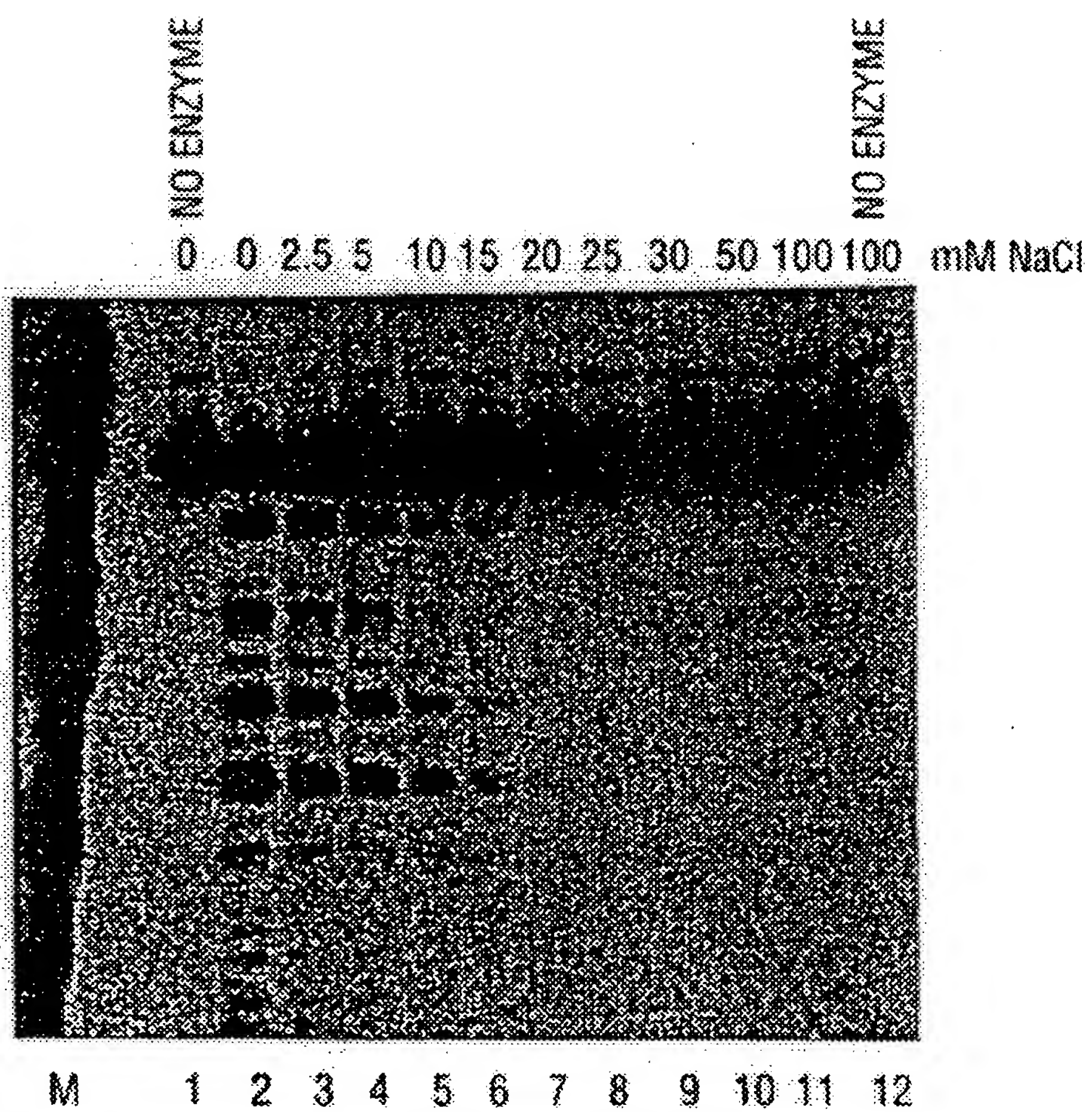


FIG. 58

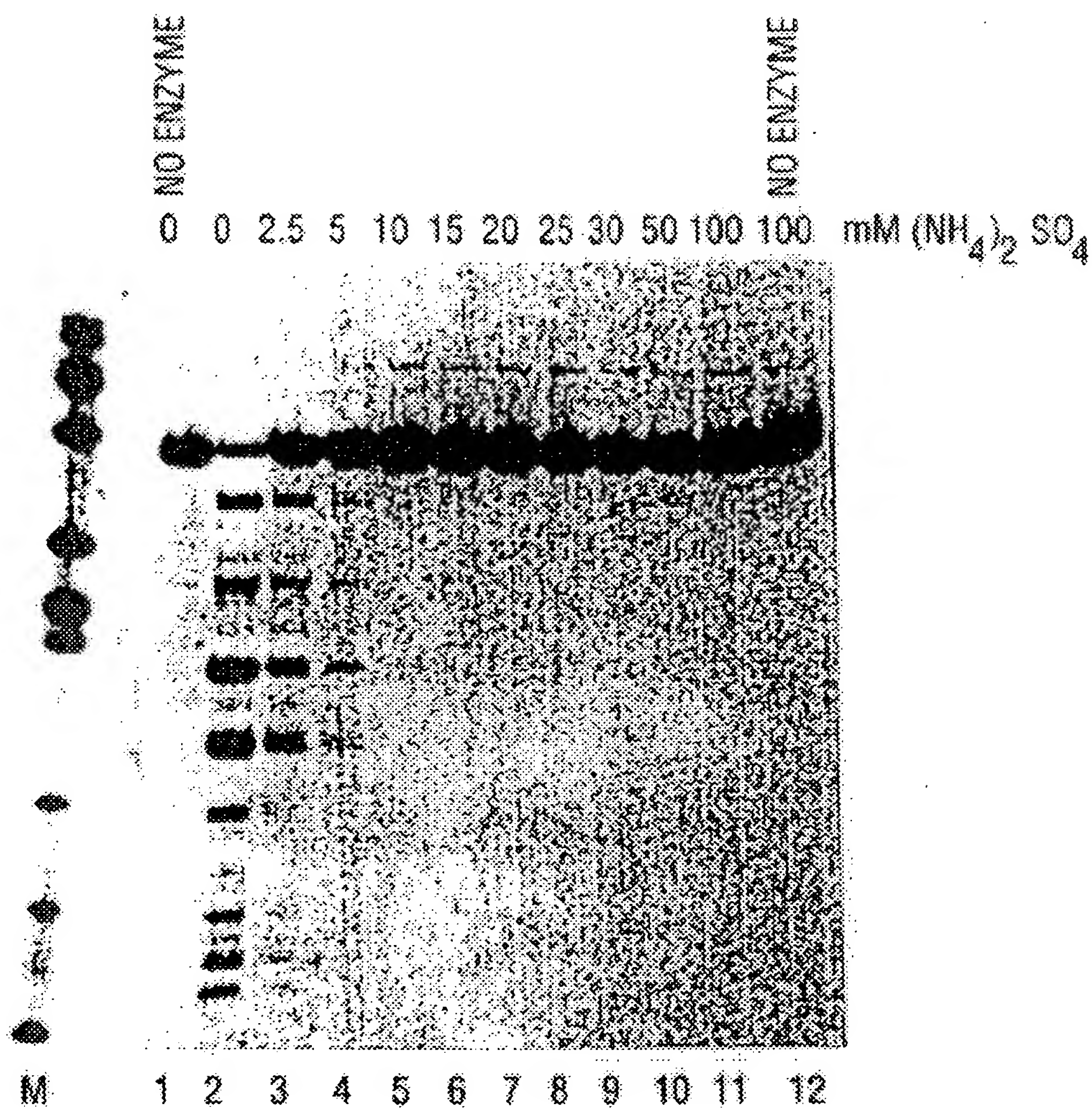


FIG. 59

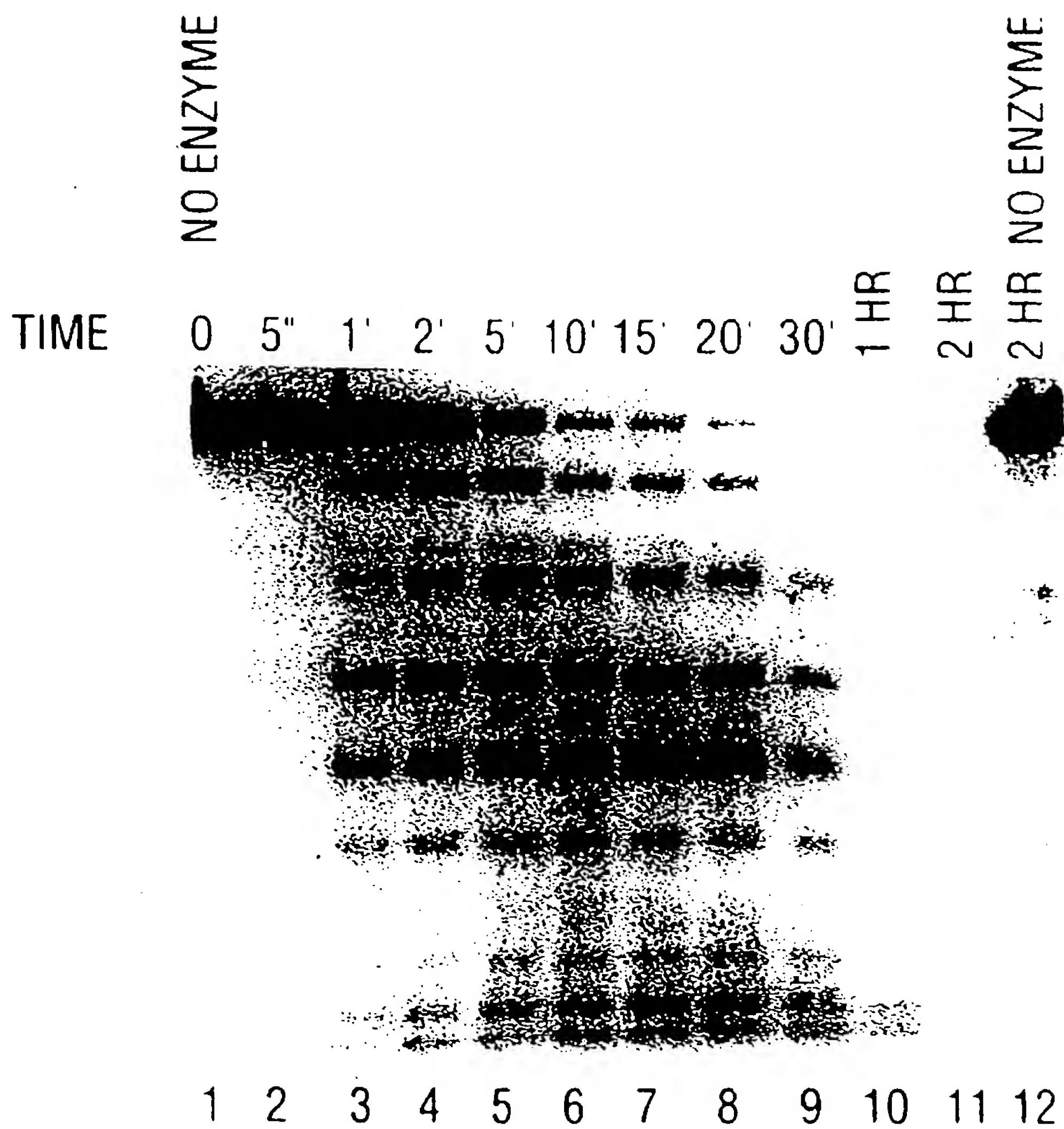


FIG. 60

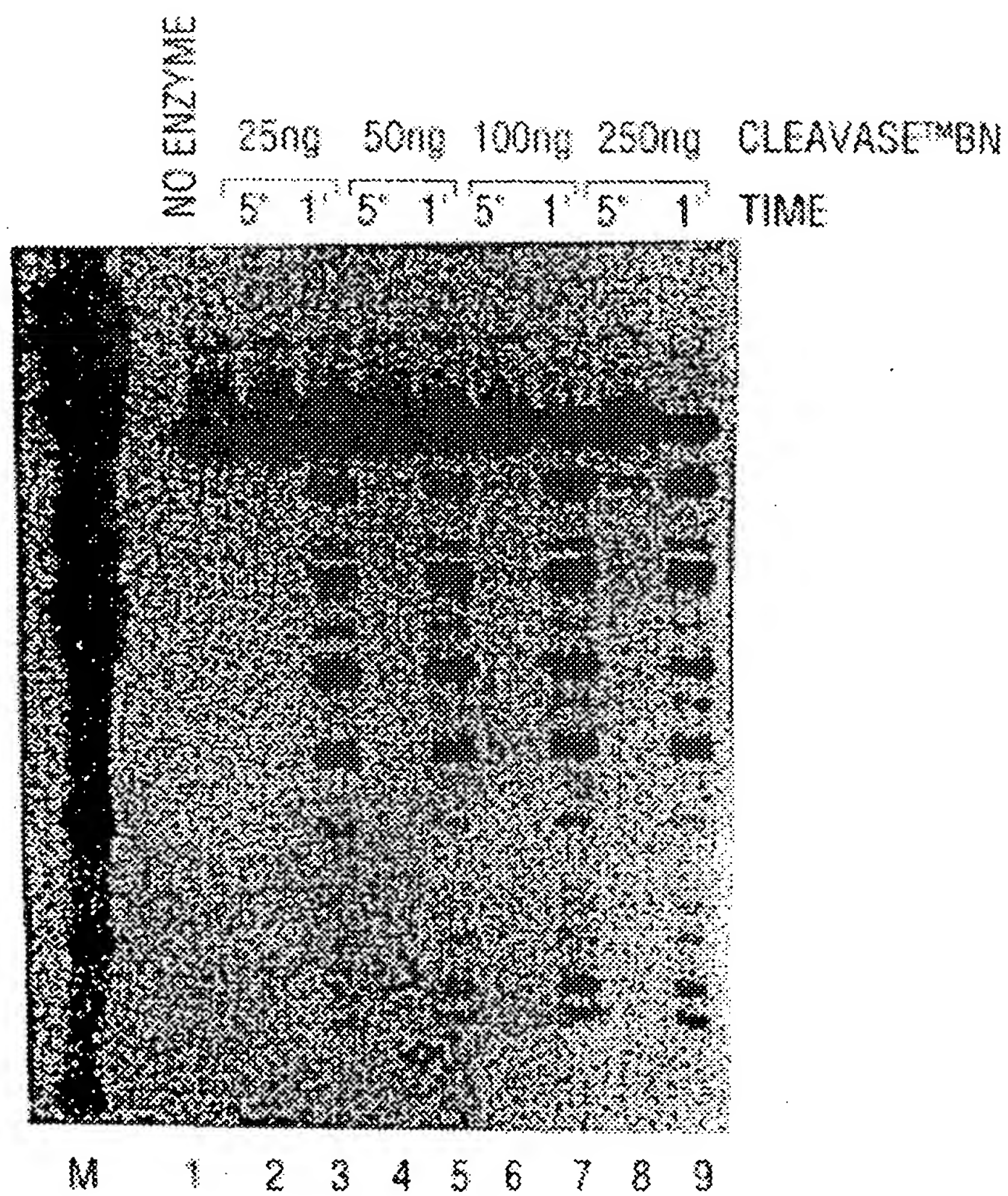


FIG. 61

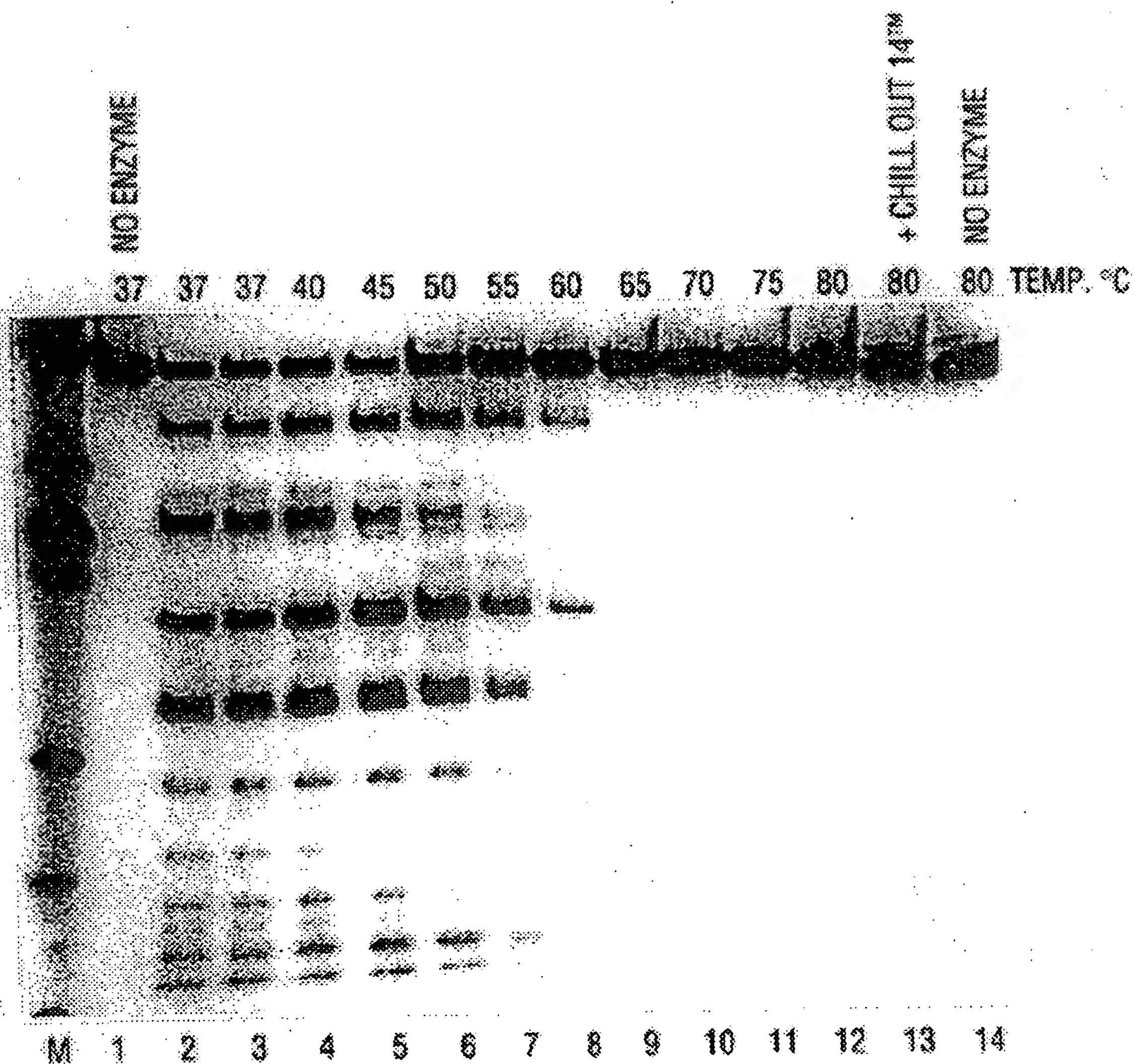


FIG. 62

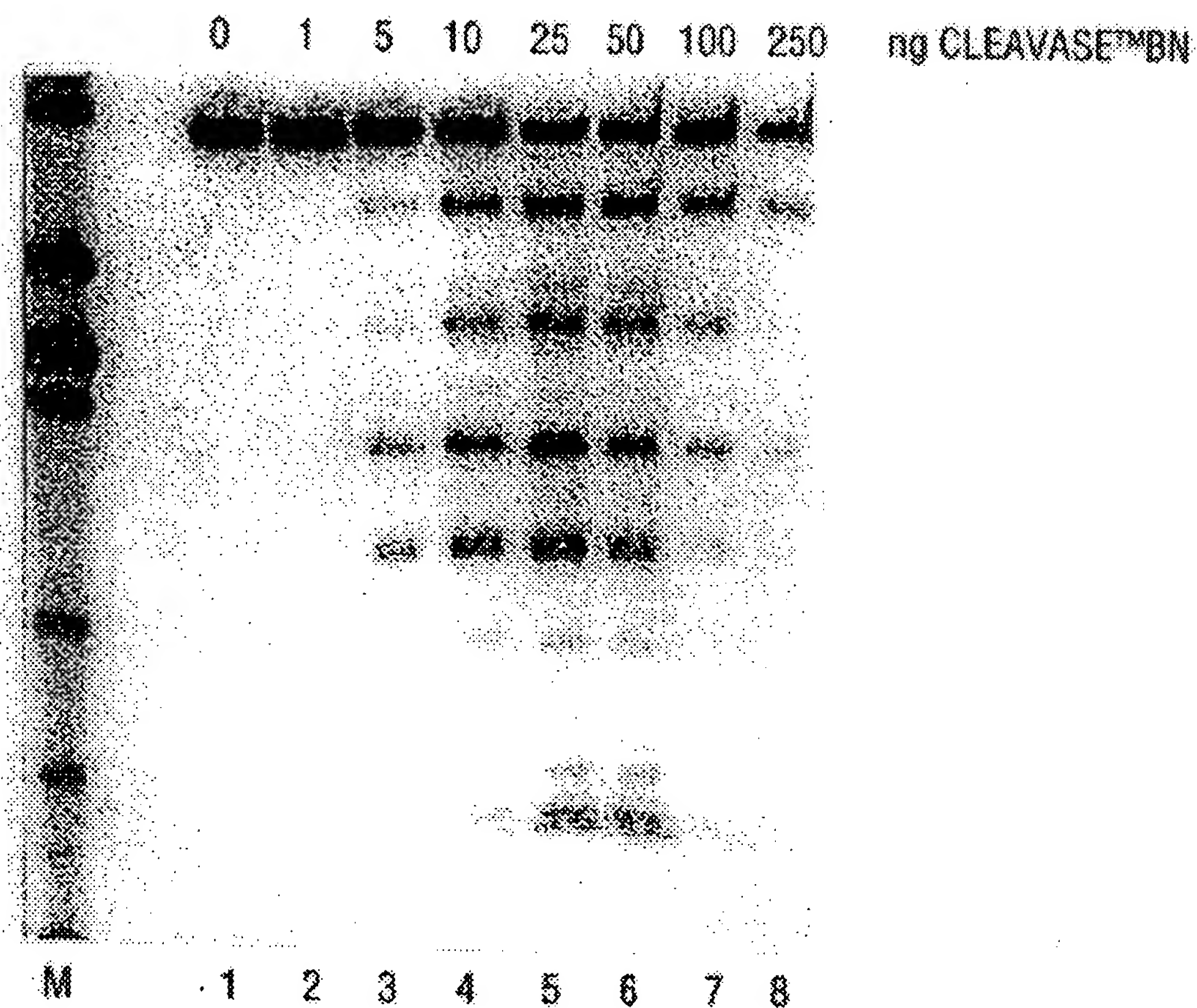


FIG. 63

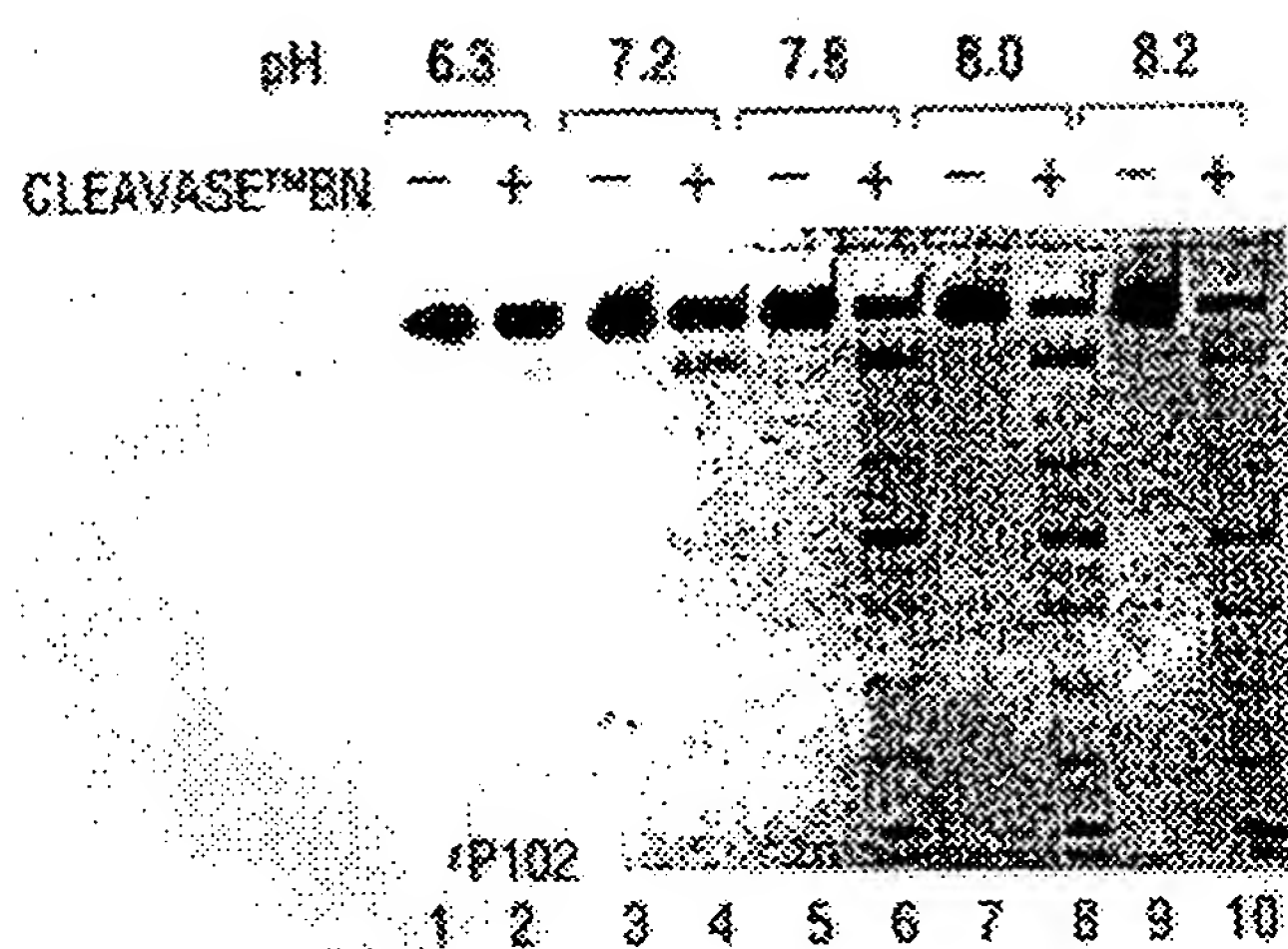


FIG. 64A

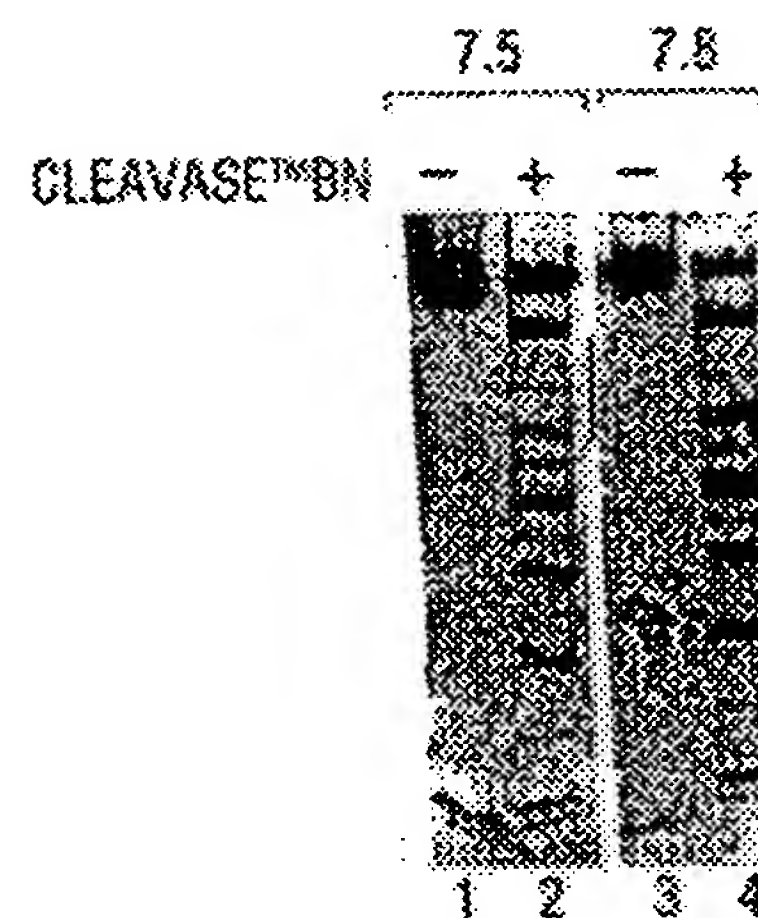


FIG. 64B

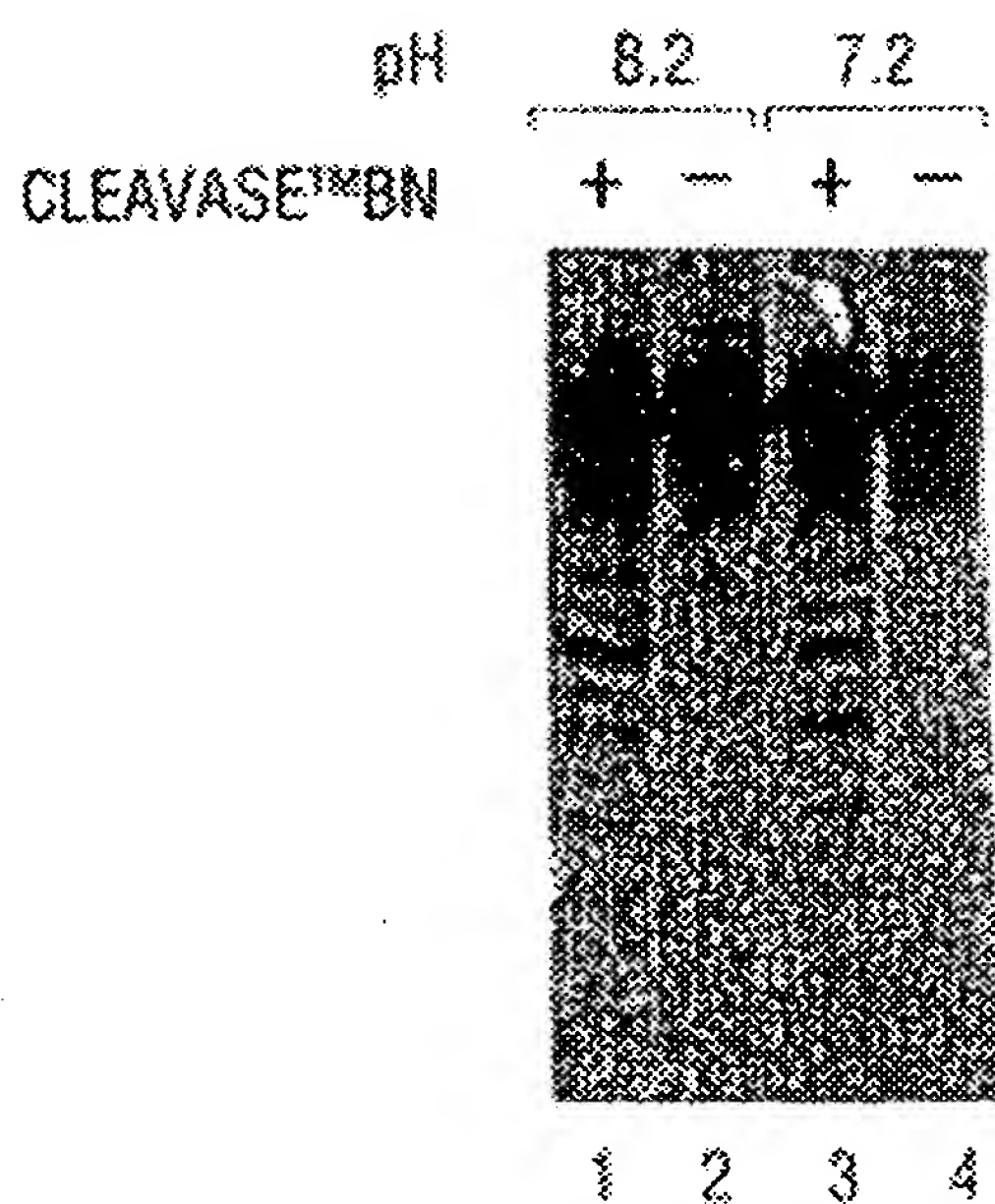


FIG. 65A

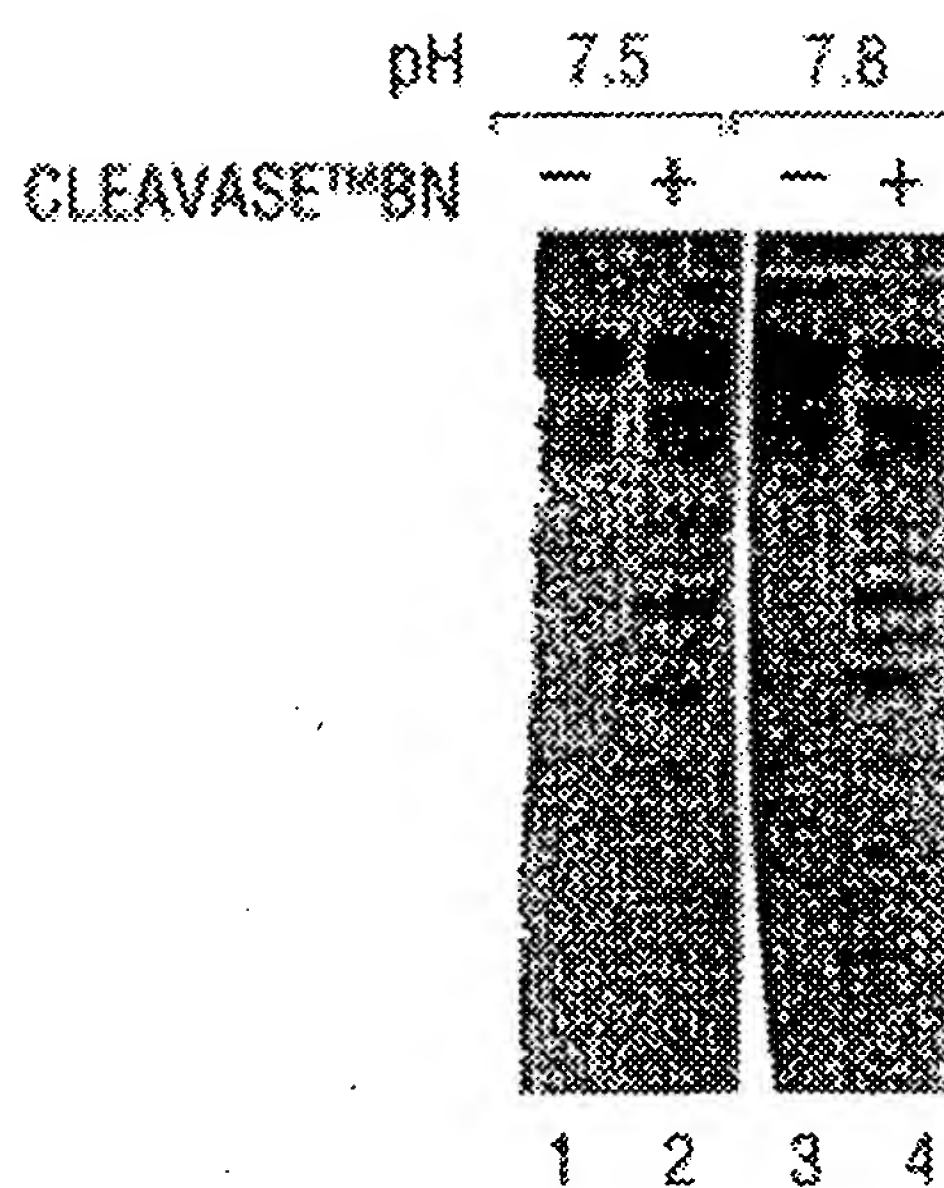


FIG. 65B

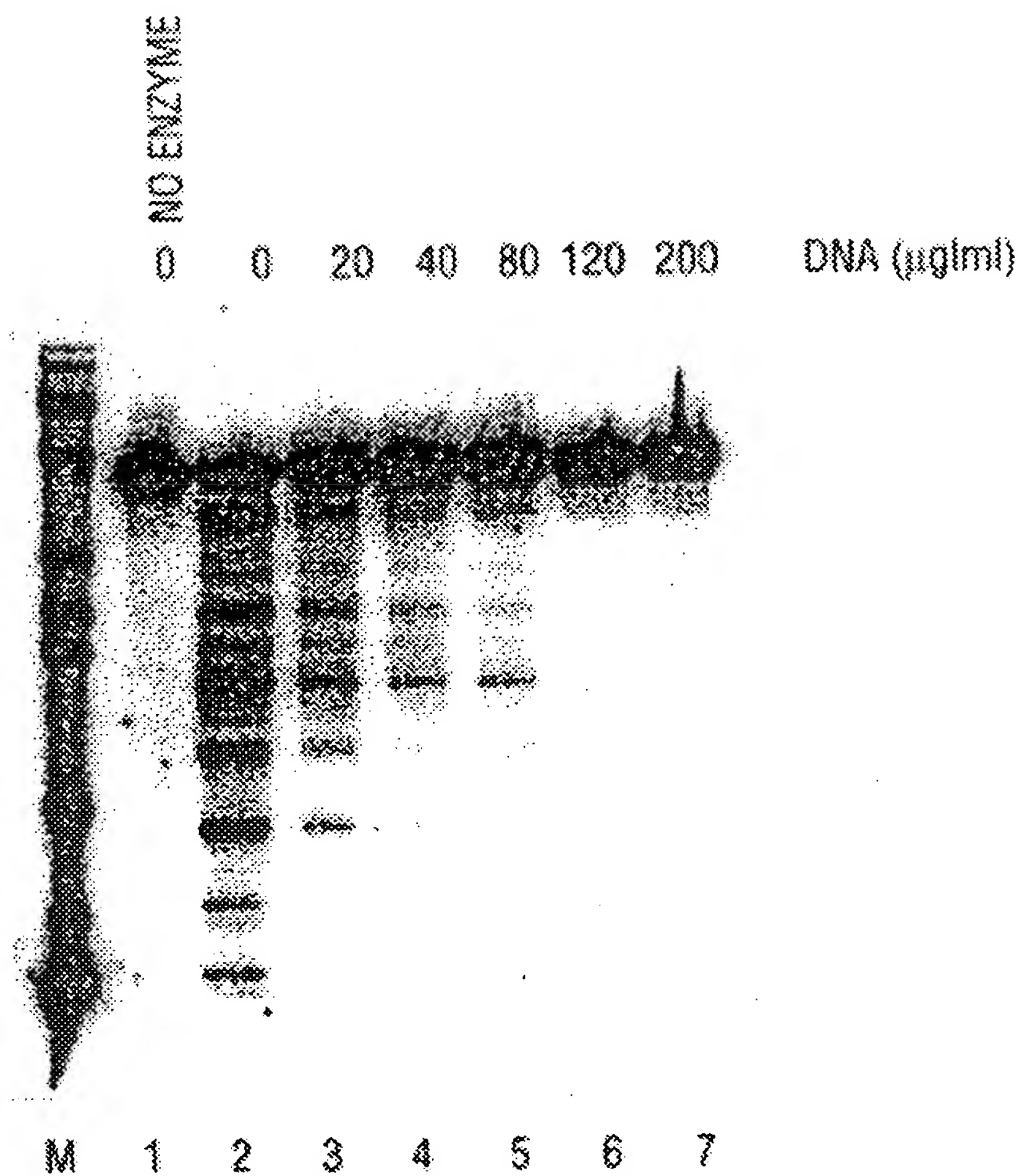


FIG. 66

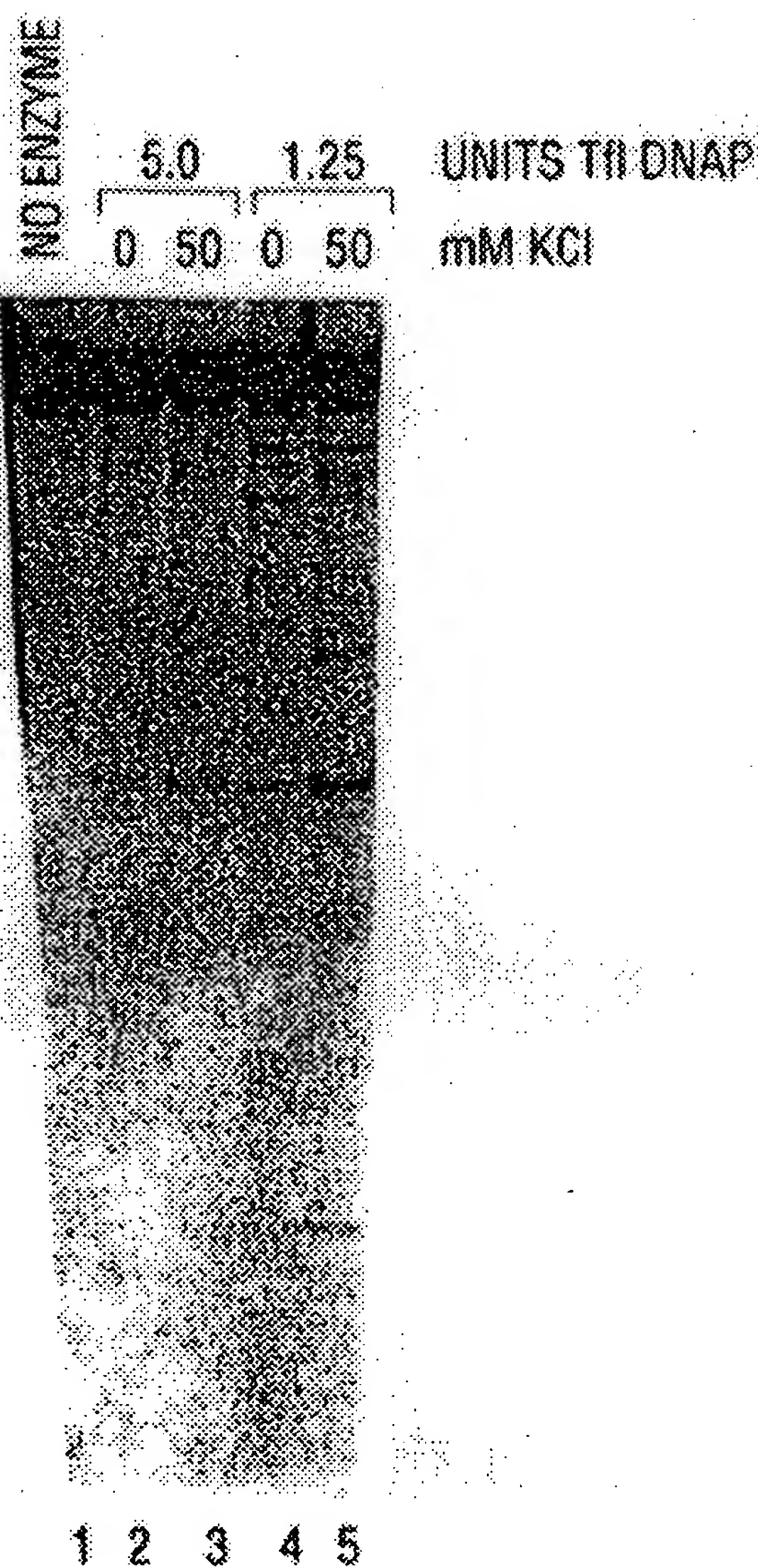


FIG. 67

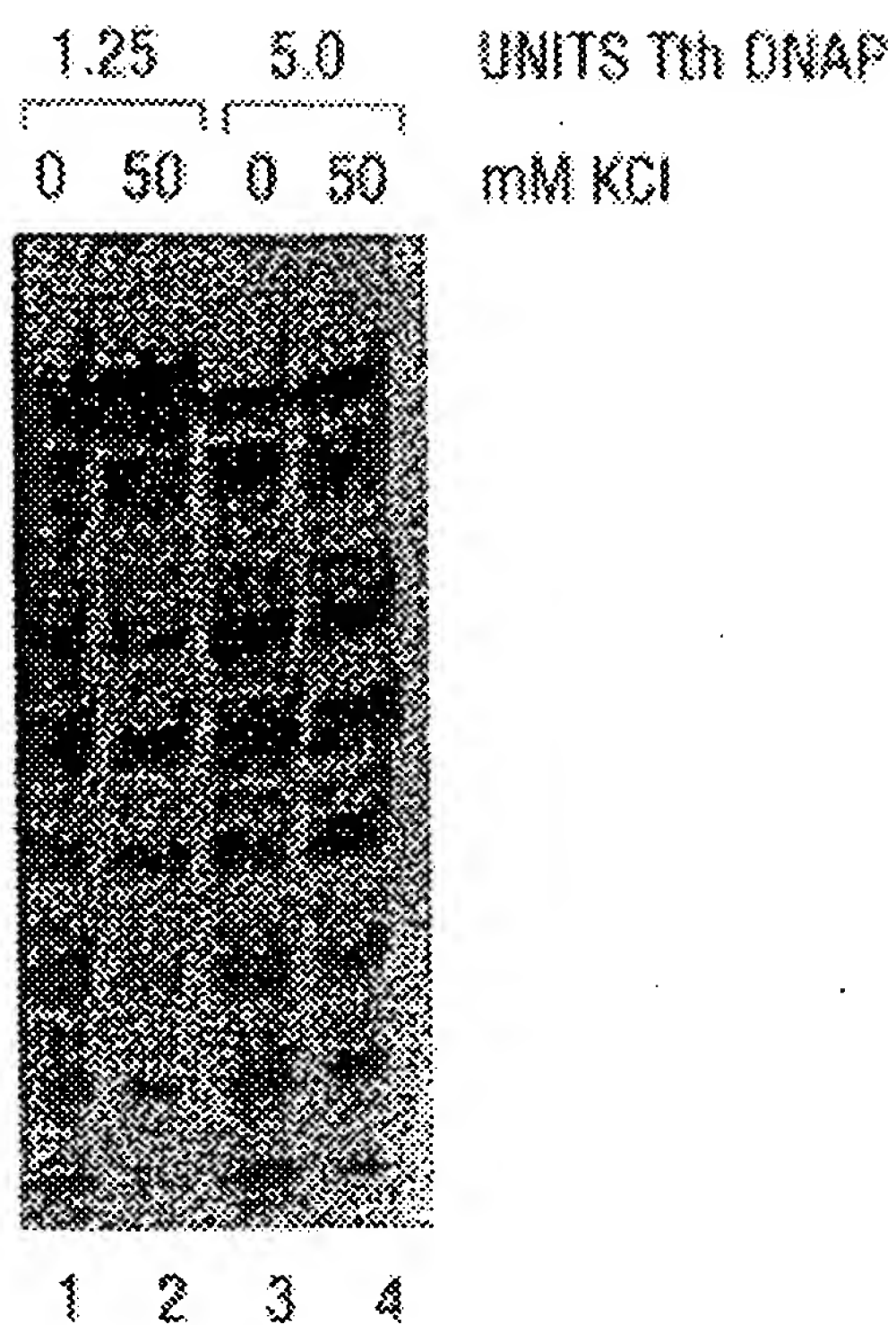


FIG. 68

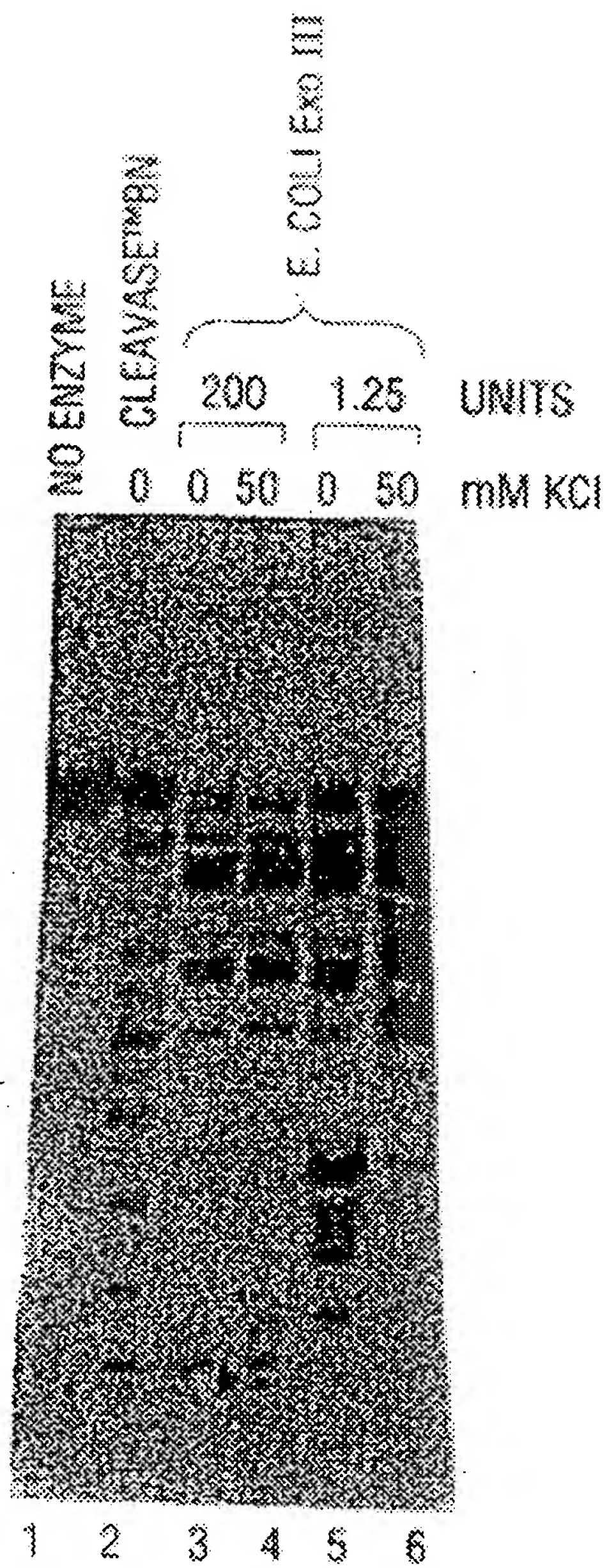


FIG. 69

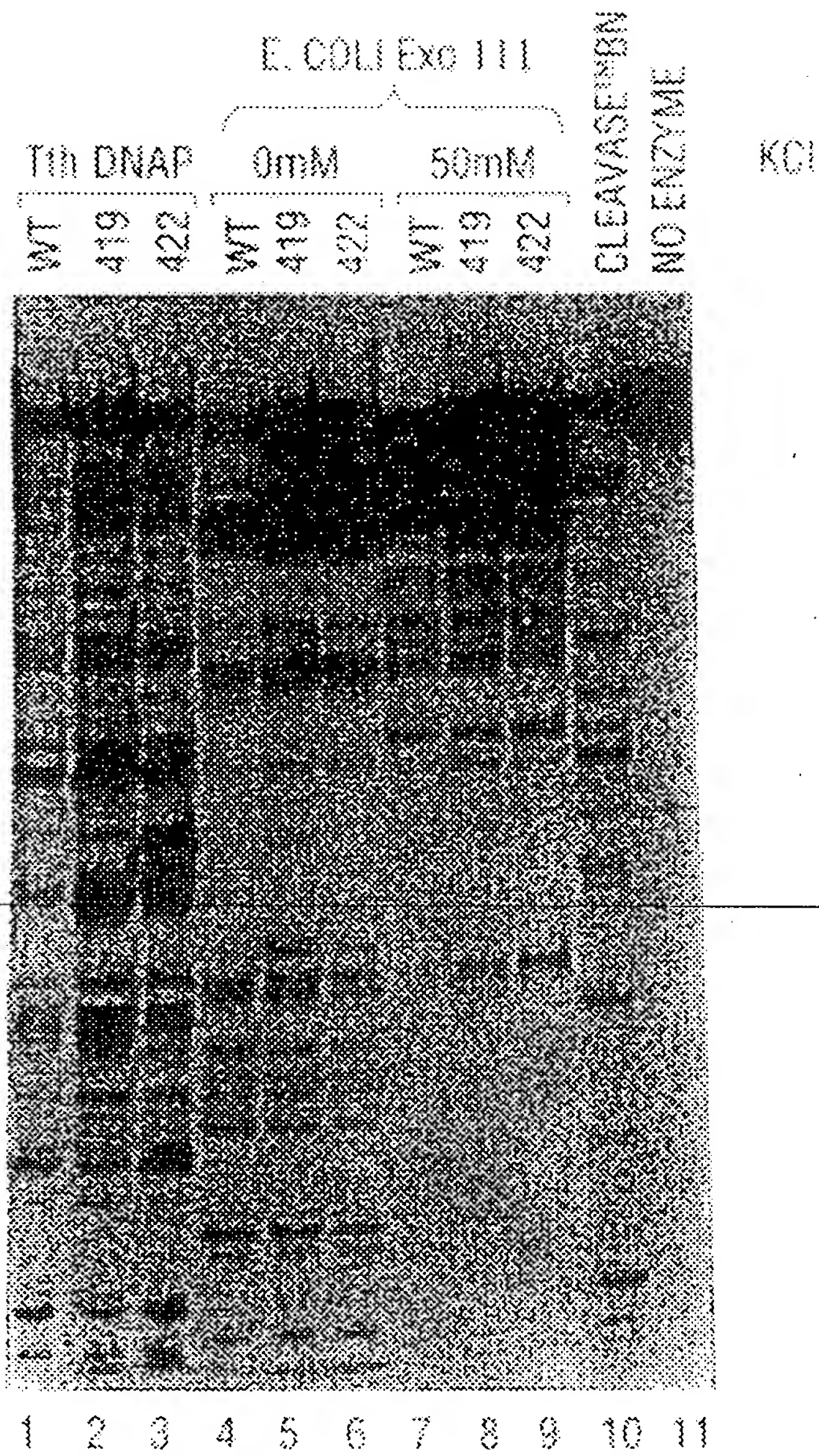
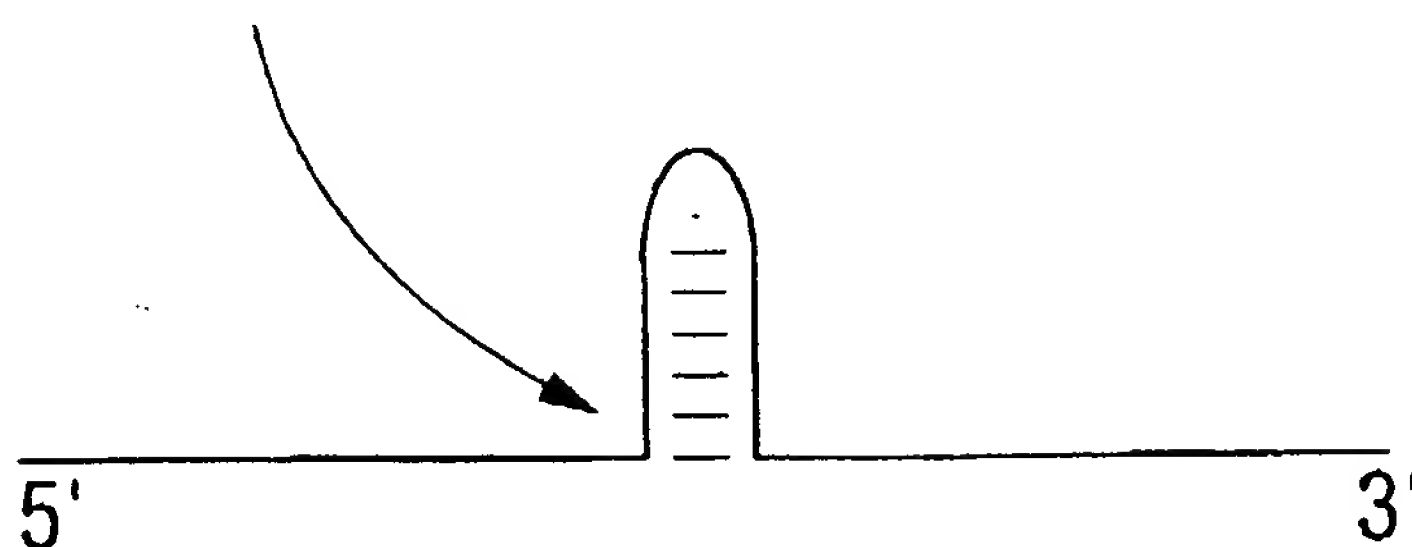


FIG. 70



5' CLEAVAGE SITE



3' CLEAVAGE SITE

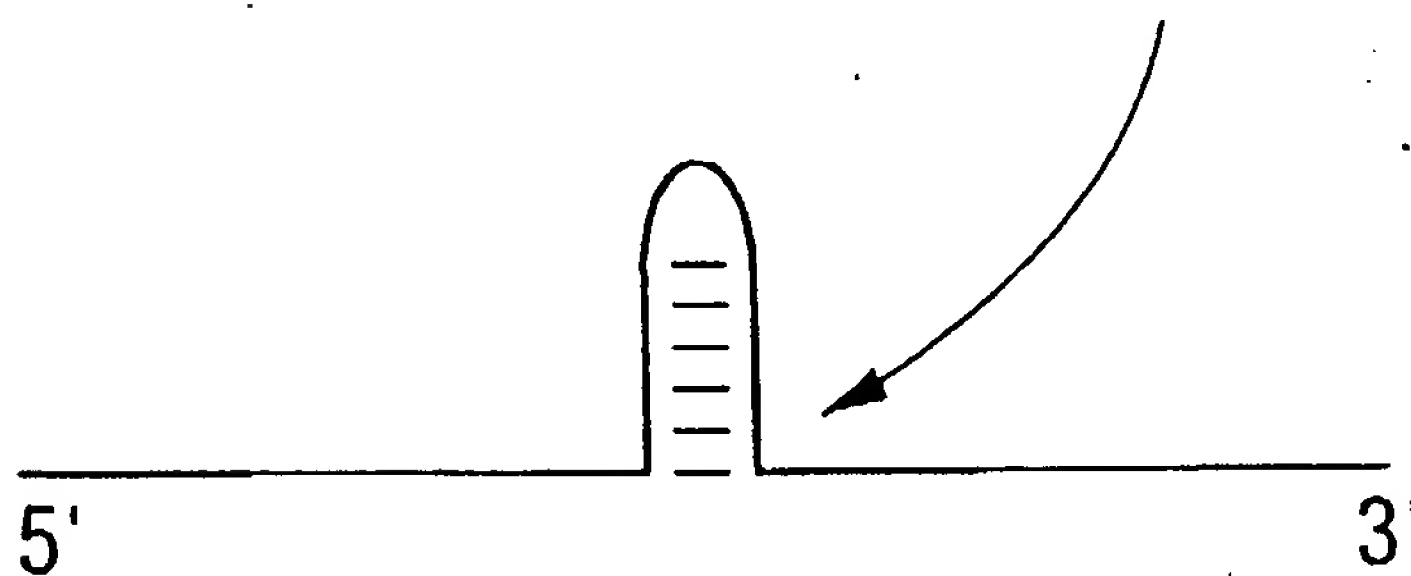


FIG. 71

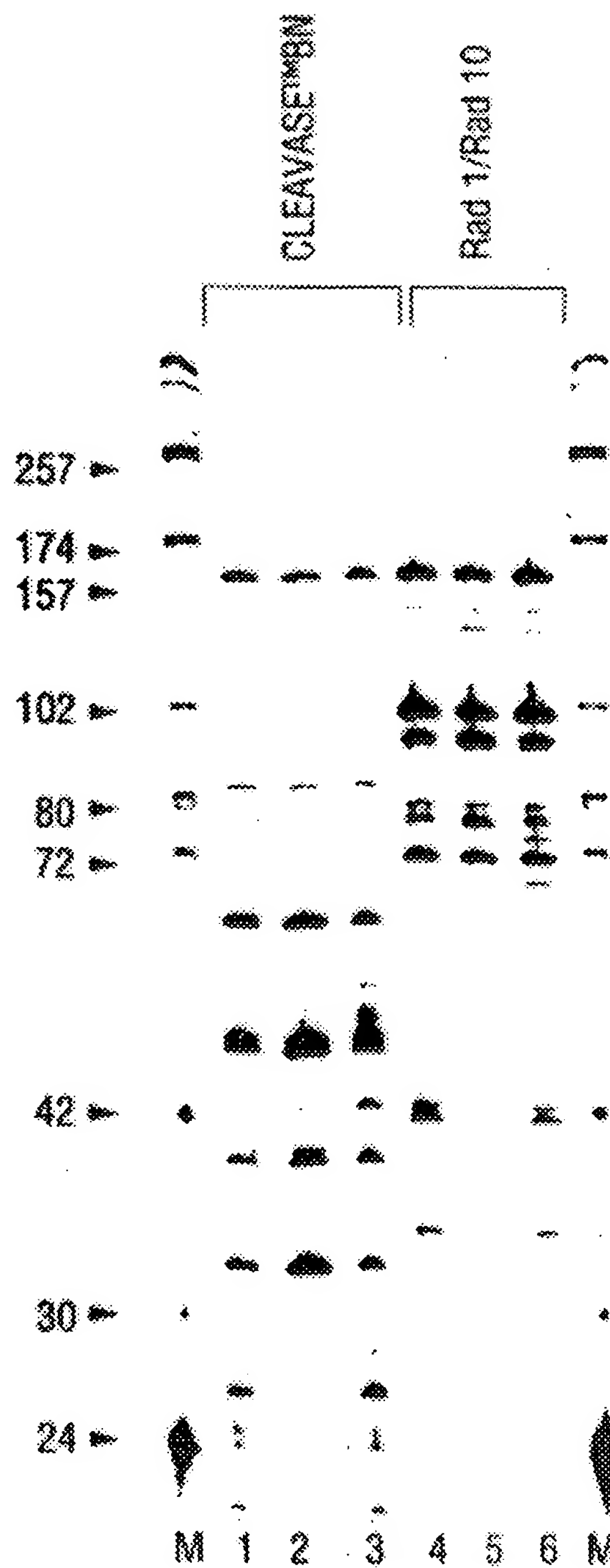


FIG. 72



174



FIG. 73

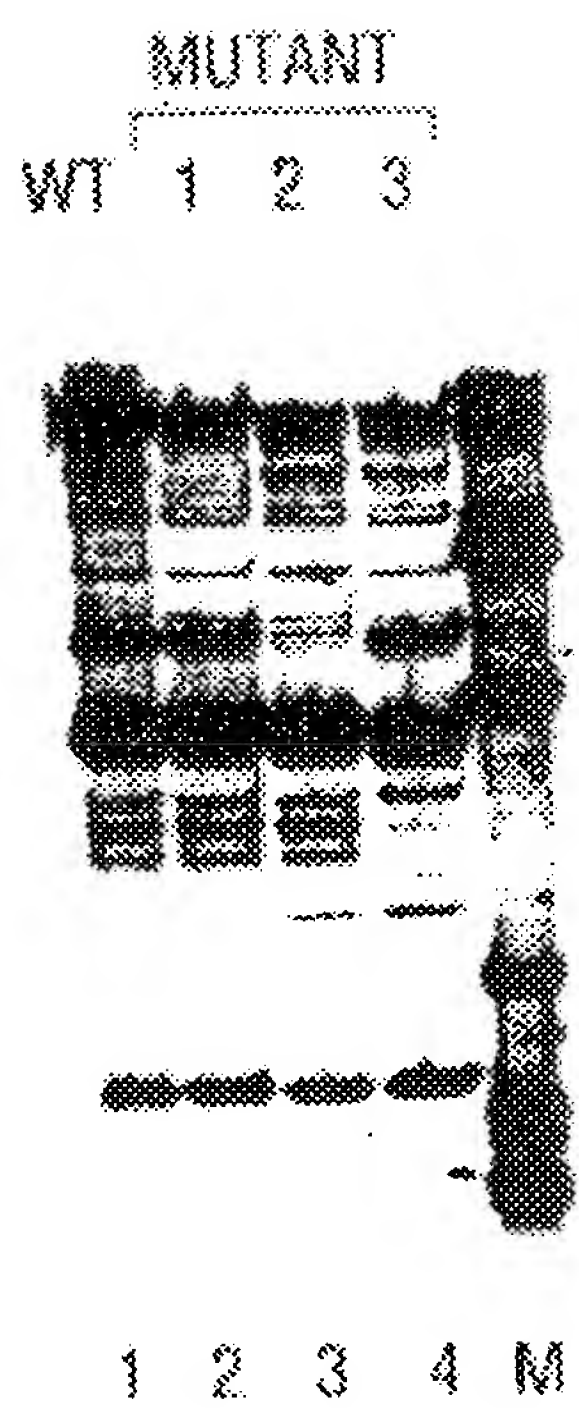


FIG. 74A

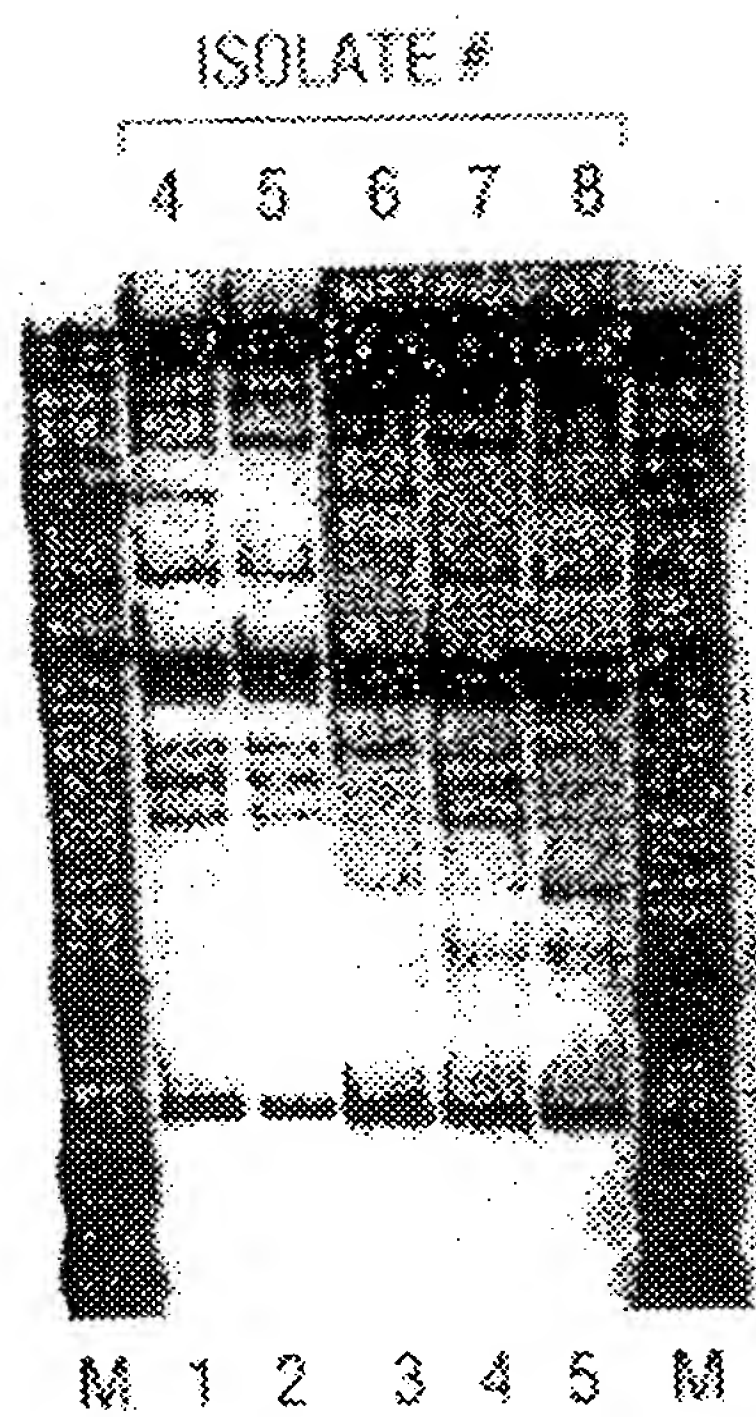


FIG. 74B

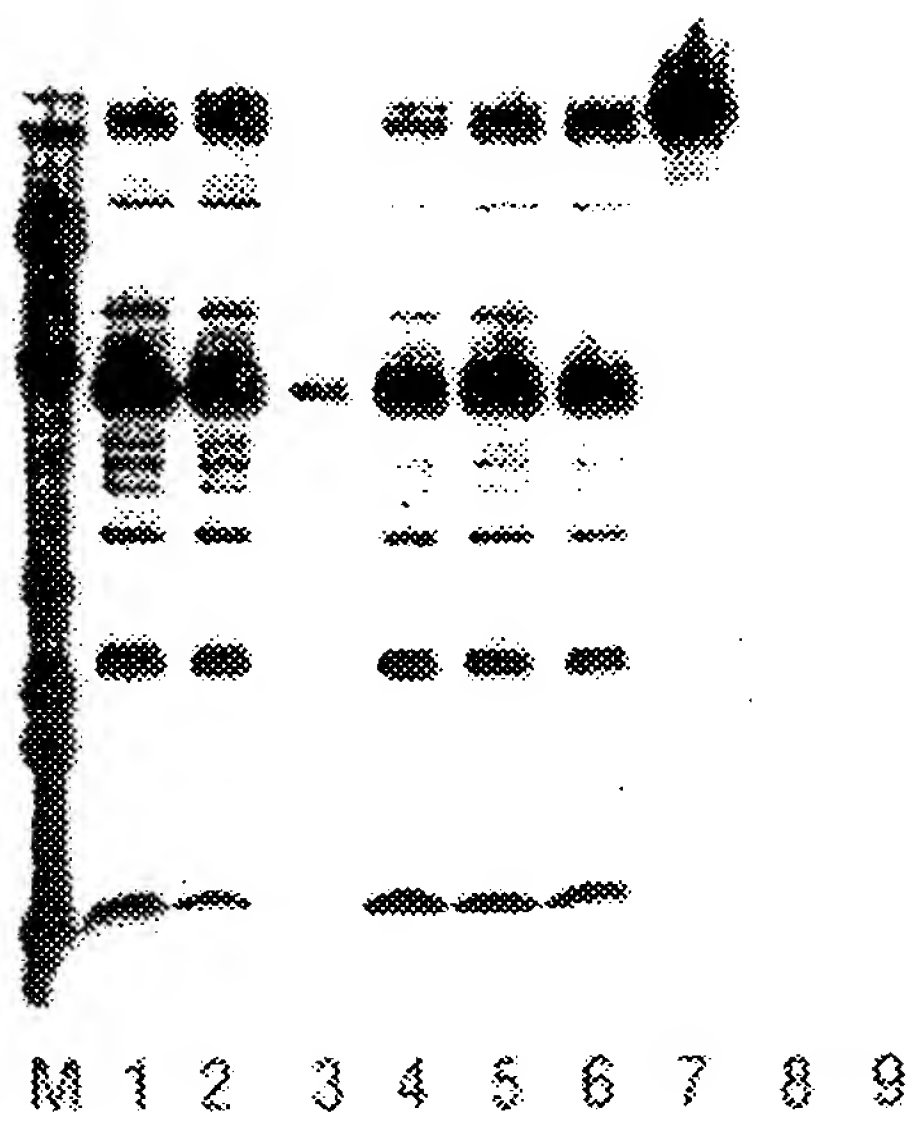


FIG. 75



% OF TOTAL
MUTATIONS

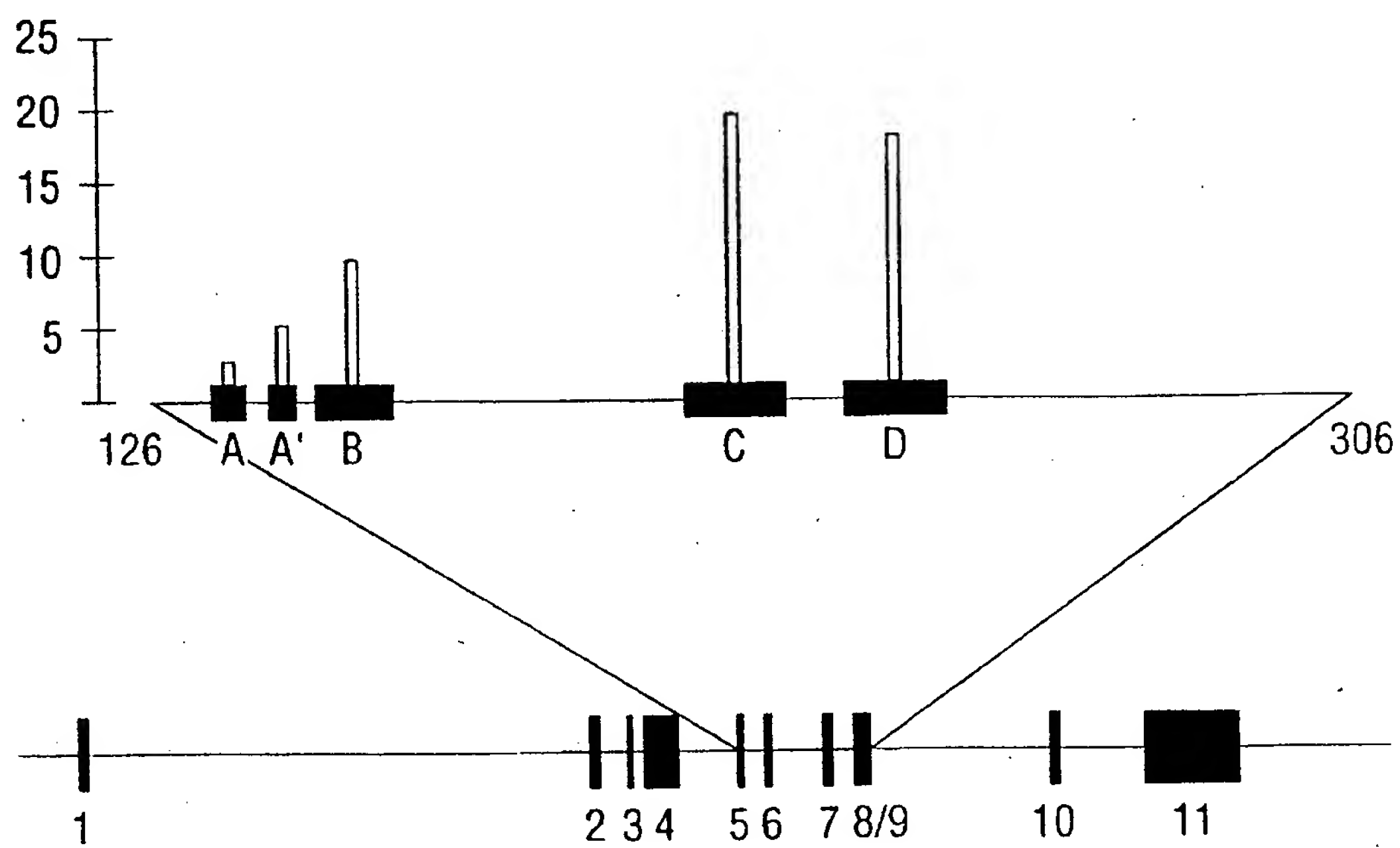
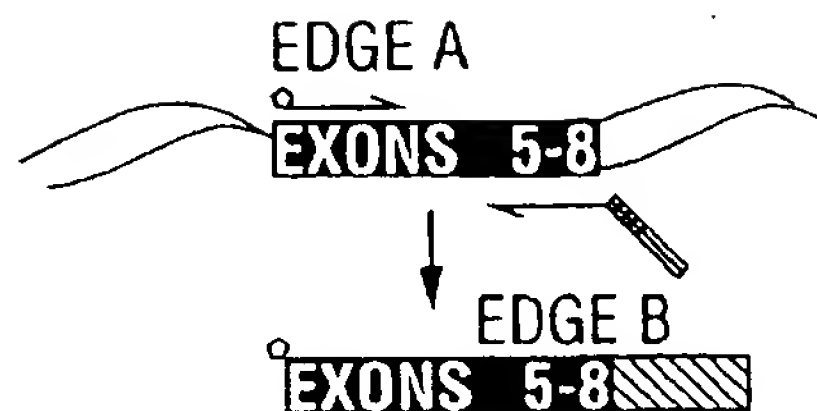


FIG. 76



PCR 1

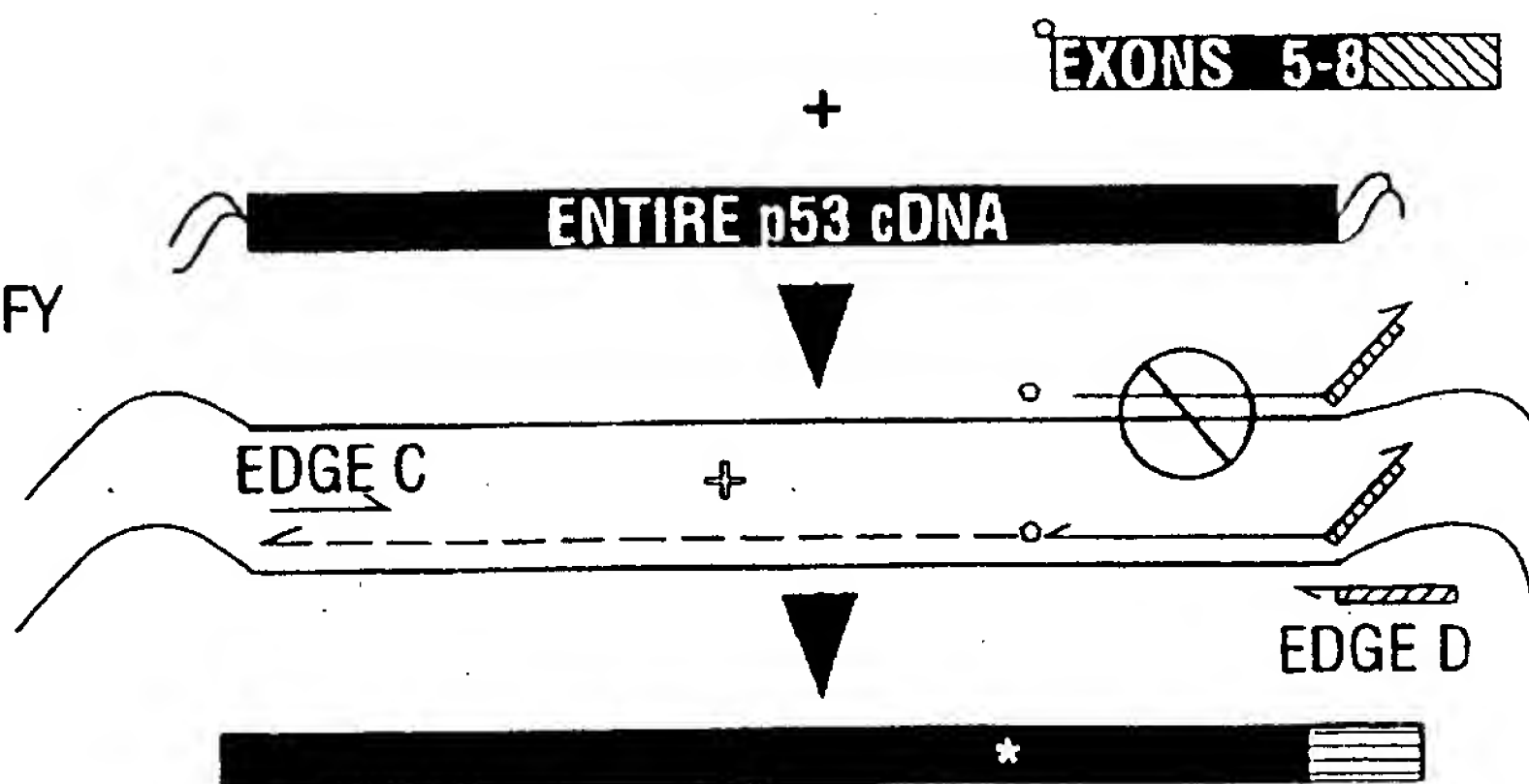
GENERATE FRAGMENT CONTAINING MUTATION



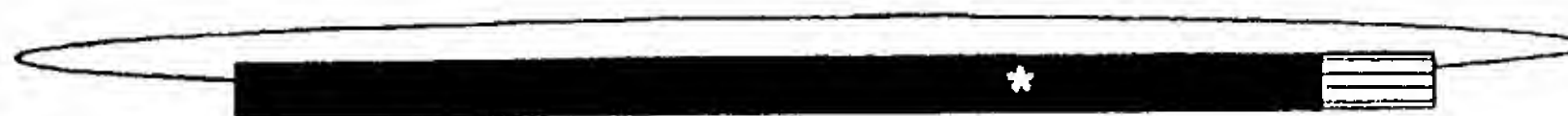
ADD AMPLIFIED FRAGMENT TO PCR 2

PCR 2

DENATURE AND AMPLIFY



INSERT MUTANT INTO FRAGMENT BY PCR



DIGEST AND CLONE INTO VECTOR



SEQUENCE AND ARCHIVE



PCR AMPLIFY EXONS 5-8

CFLP ANALYSIS OF EXONS 5-8

* EXONS 5-8

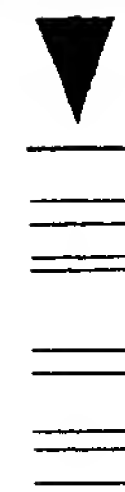


FIG. 77

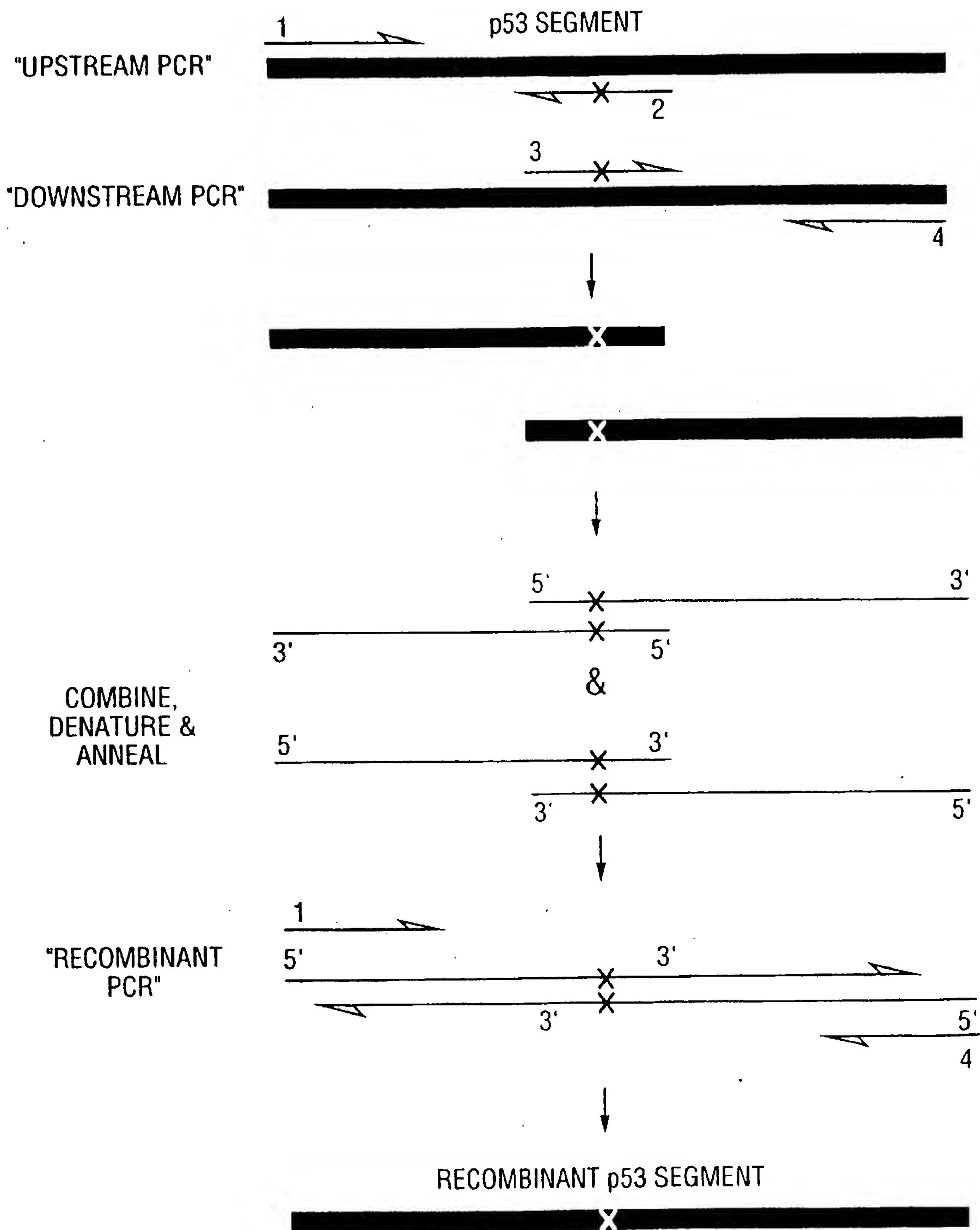


FIG. 78

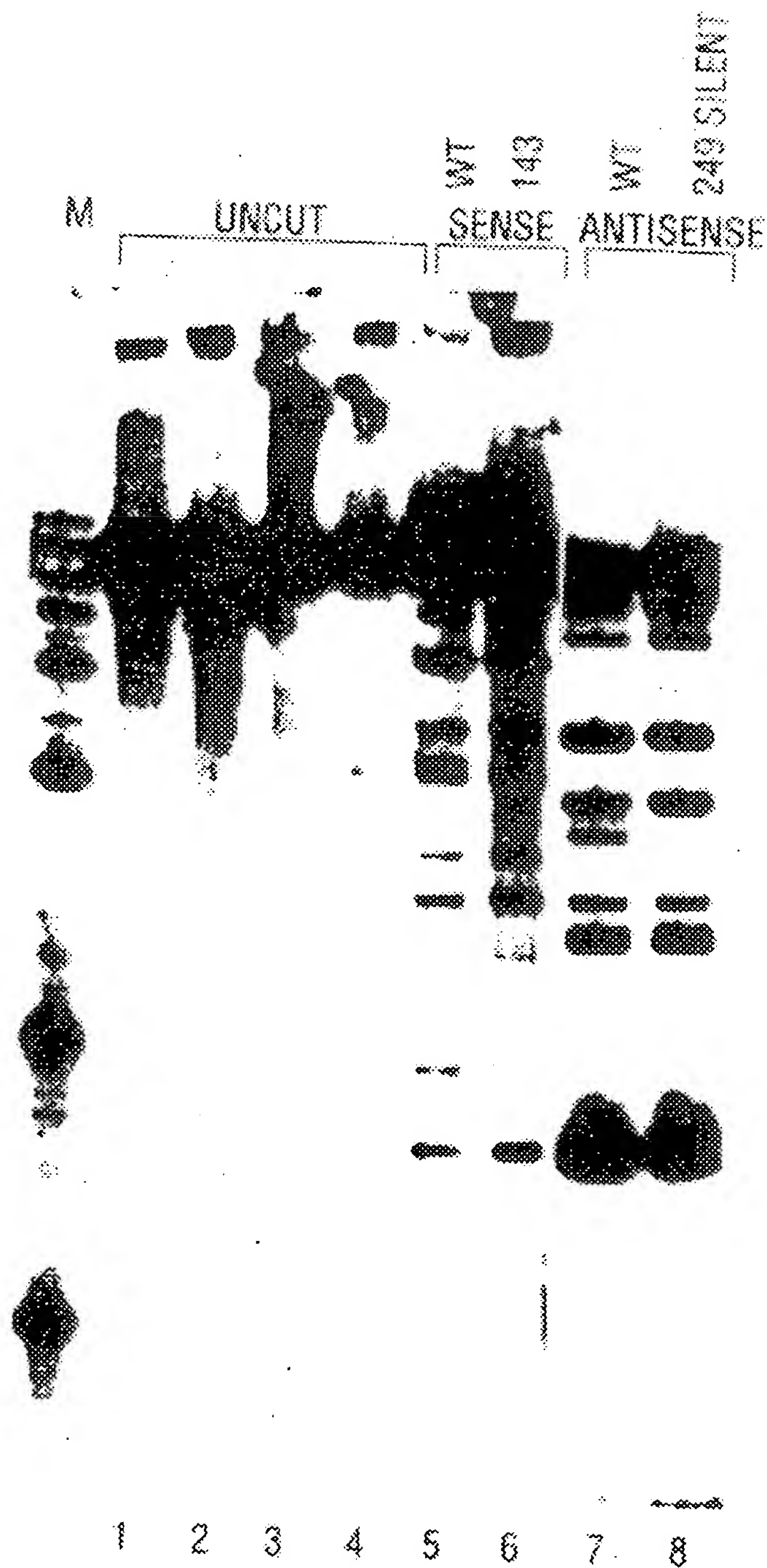


FIG. 79

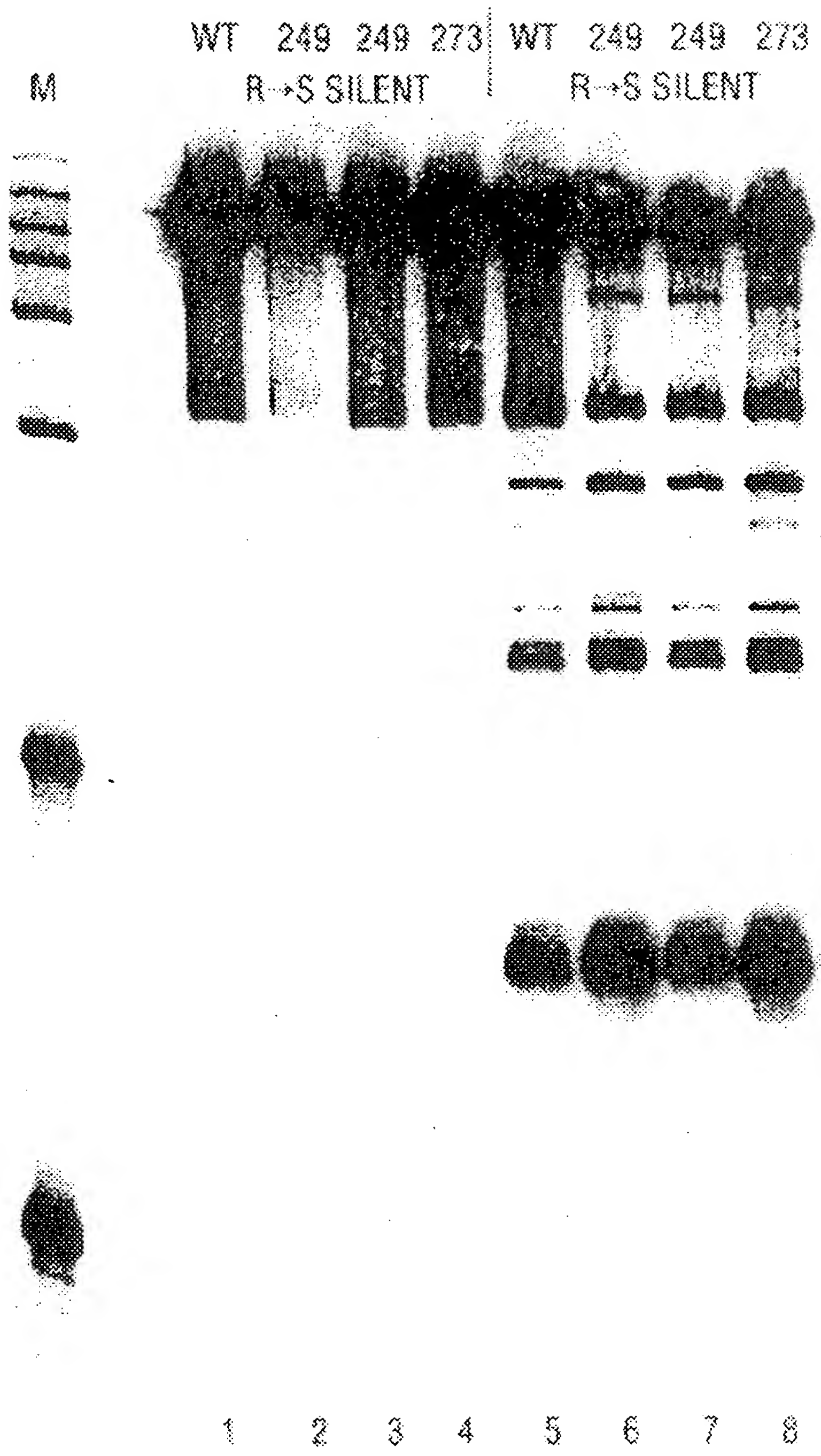


FIG. 80

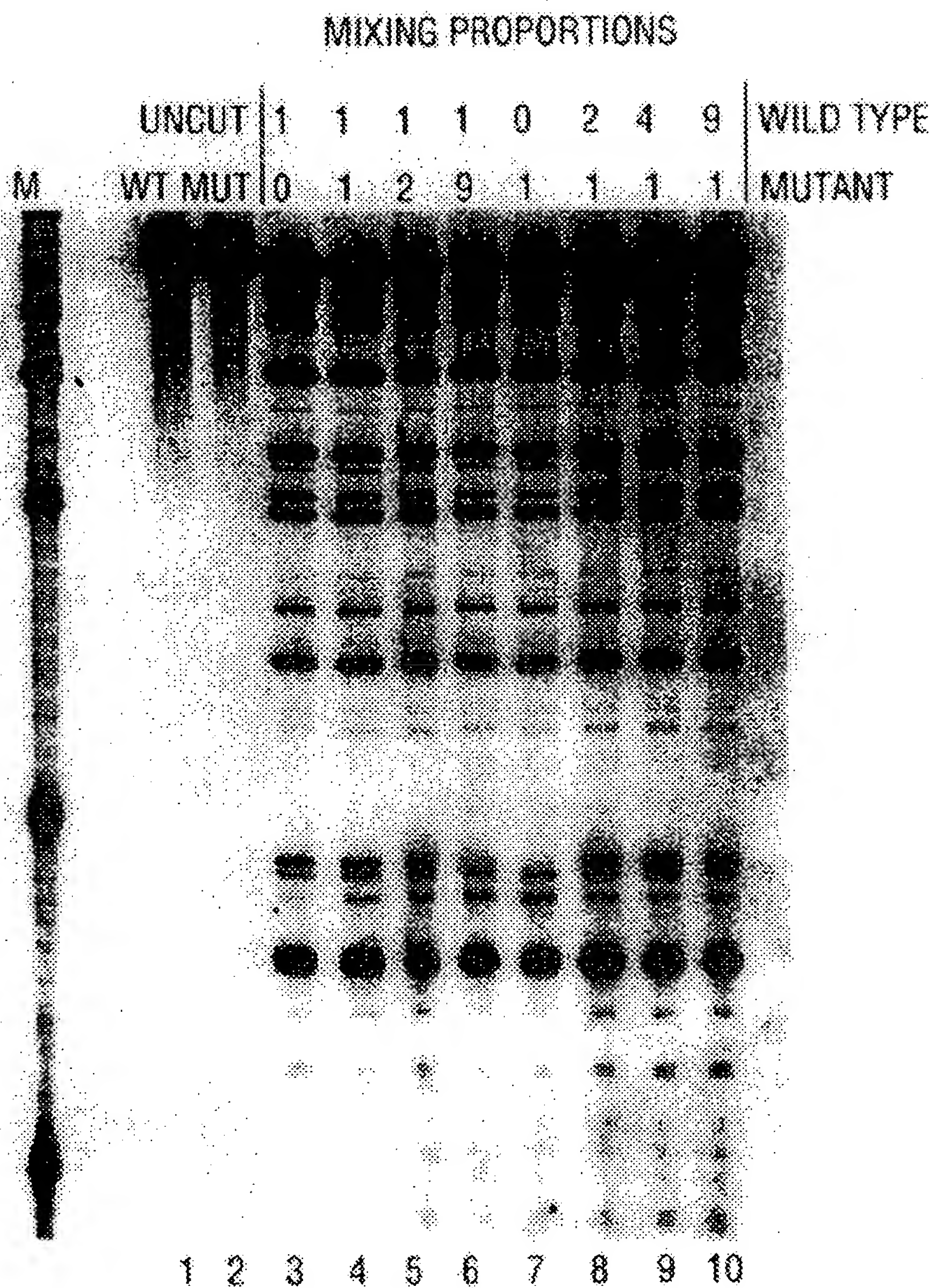


FIG. 81



HCV1.1	(SEQ ID NO:121)	1	CTGTCTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGT <u>A</u>	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCAC	GCAGAAAGCG	<u>C</u> TAGCCATG	GCGTTAGT <u>A</u> <u>C</u>	GAGTGTCGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	G <u>I</u> CCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GCCCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	G <u>A</u> CCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT- <u>A</u> AA	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	<u>G</u> TTGGAT <u>G</u> IAA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	<u>C</u> GGGA <u>A</u> GACT	GGTCCCTTTC	TTGGAT- <u>A</u> AA	
HCV7.1			GGTGAGTACA	CCGGAATCGC	<u>T</u> GGG <u>I</u> GACC	GGTCCCTTTC	TTGGAG-CAA	

FIG. 82A



HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGGTGC	CCCCGCGAGA	ICACTAGCCG	
HCVI.1	201	AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCVI.1	251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

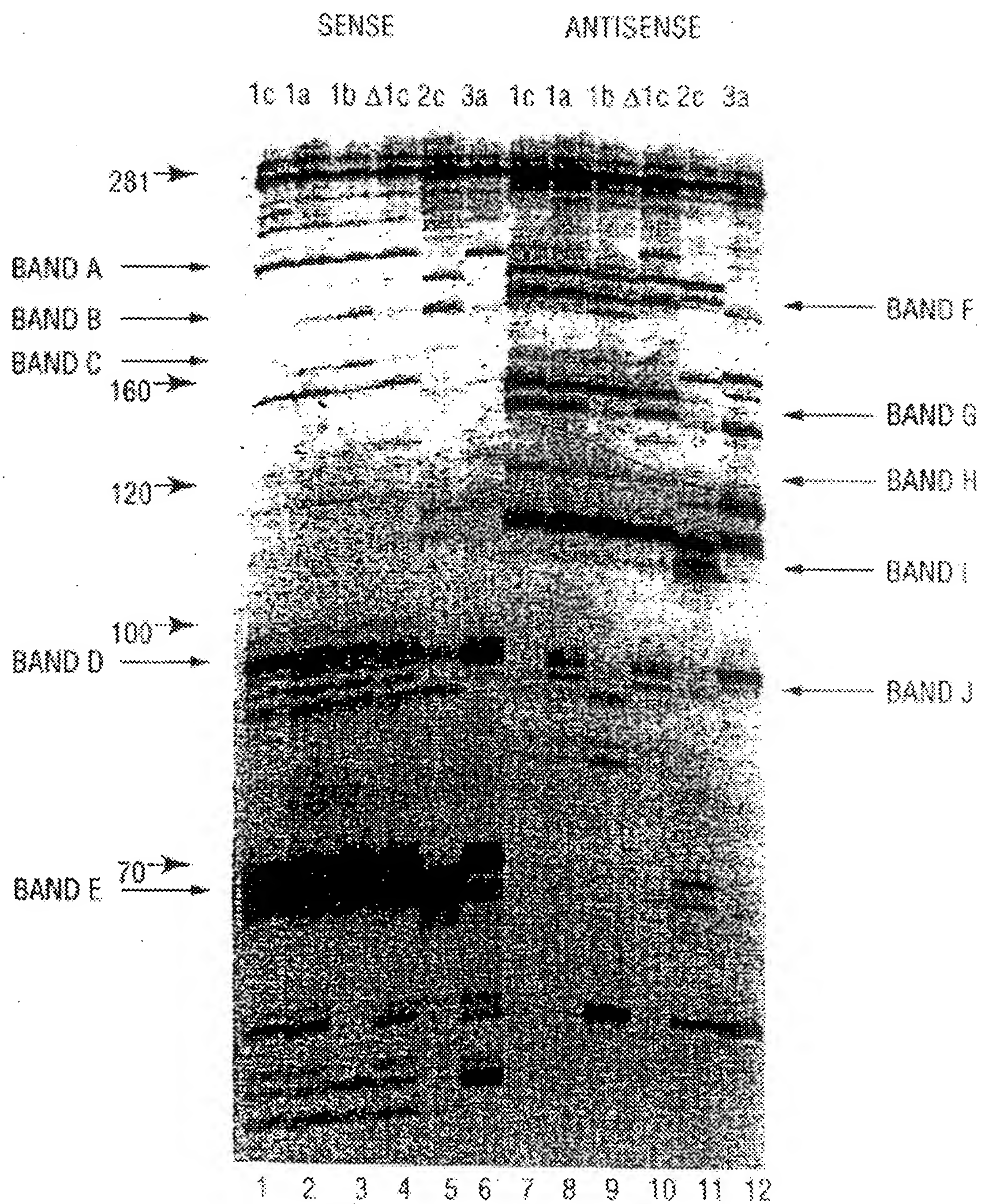


FIG. 83

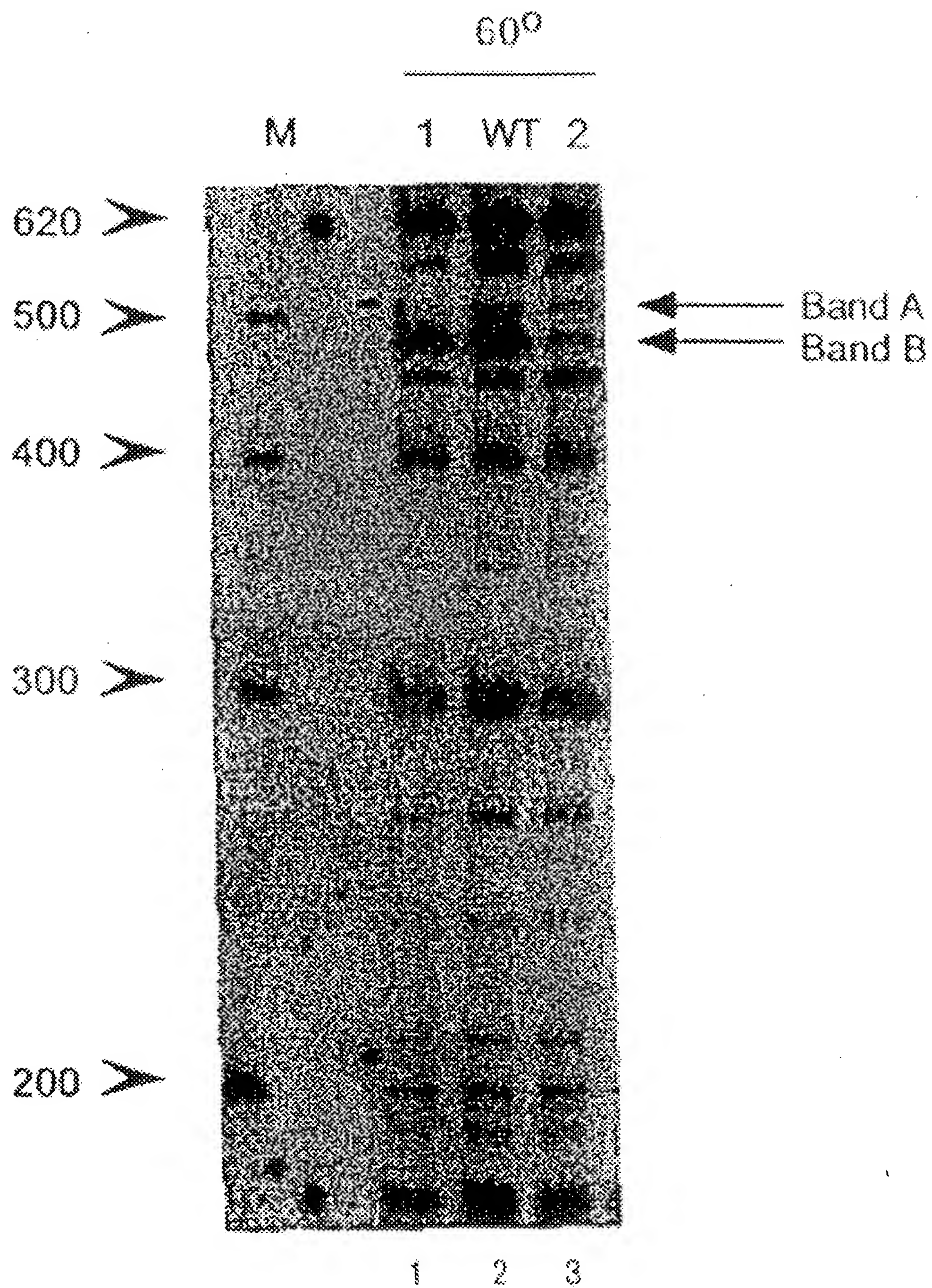


FIG. 84

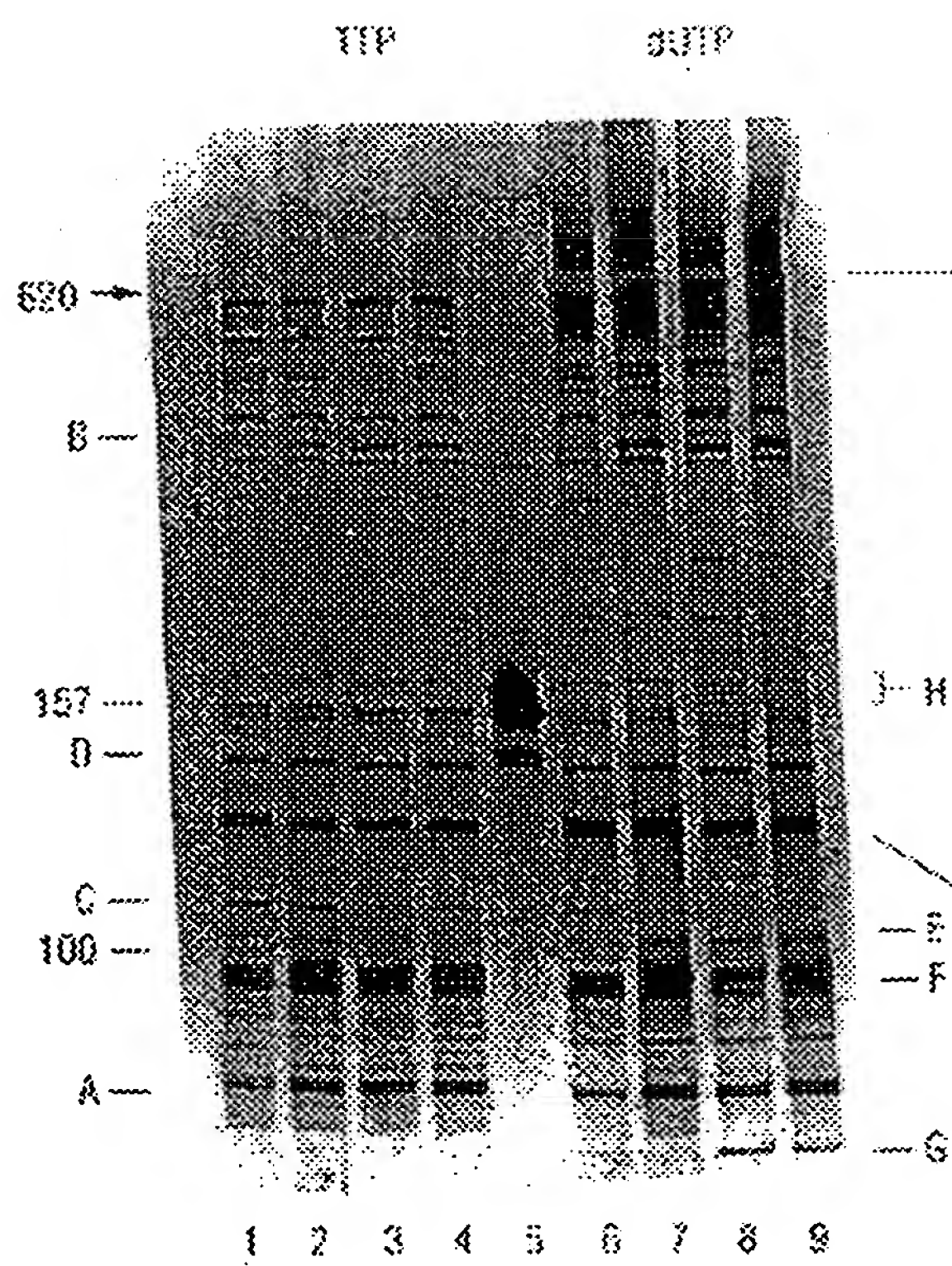


FIG. 85A

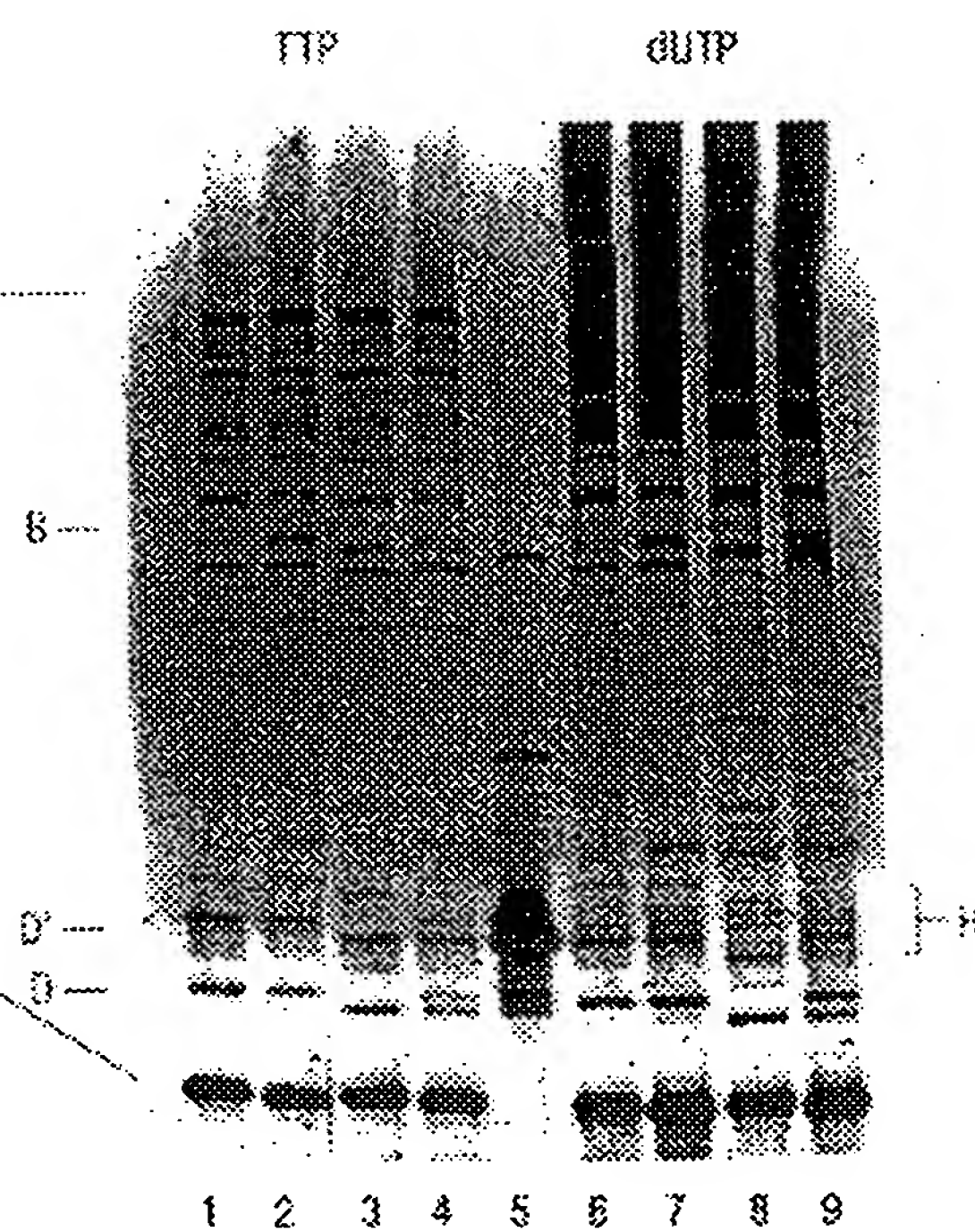


FIG. 85B

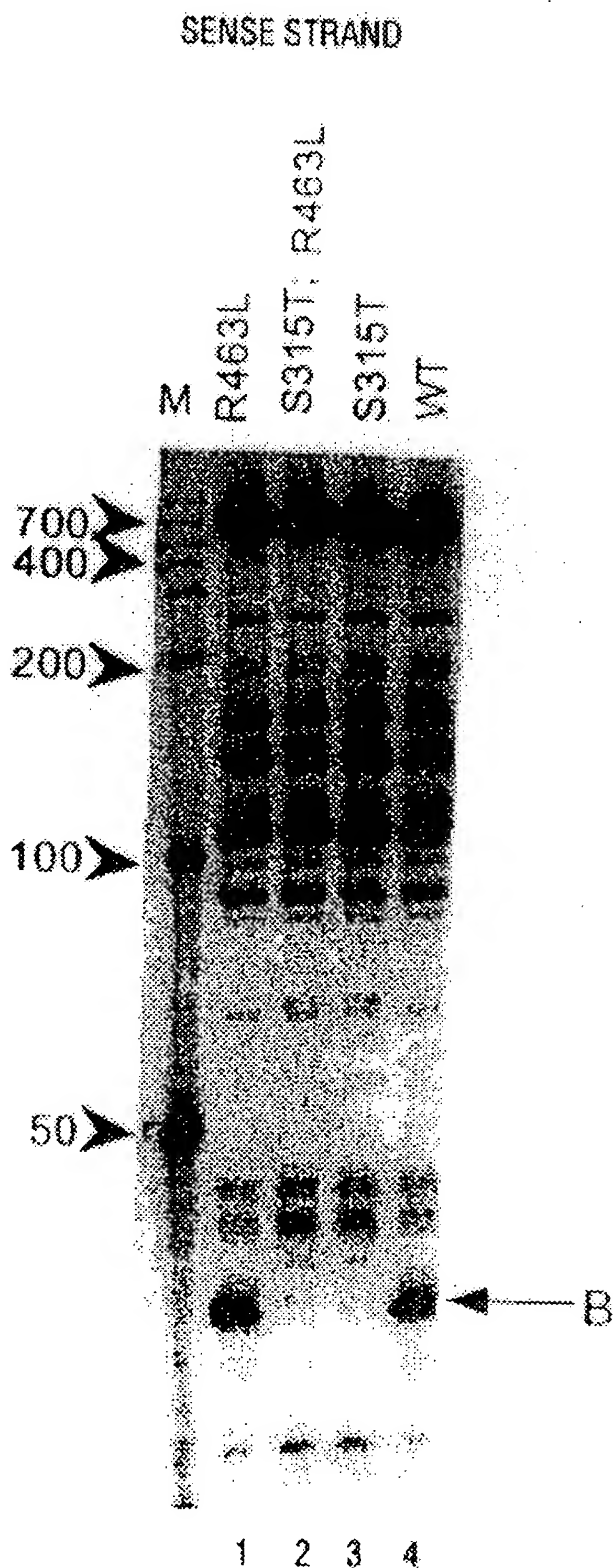


FIG. 86

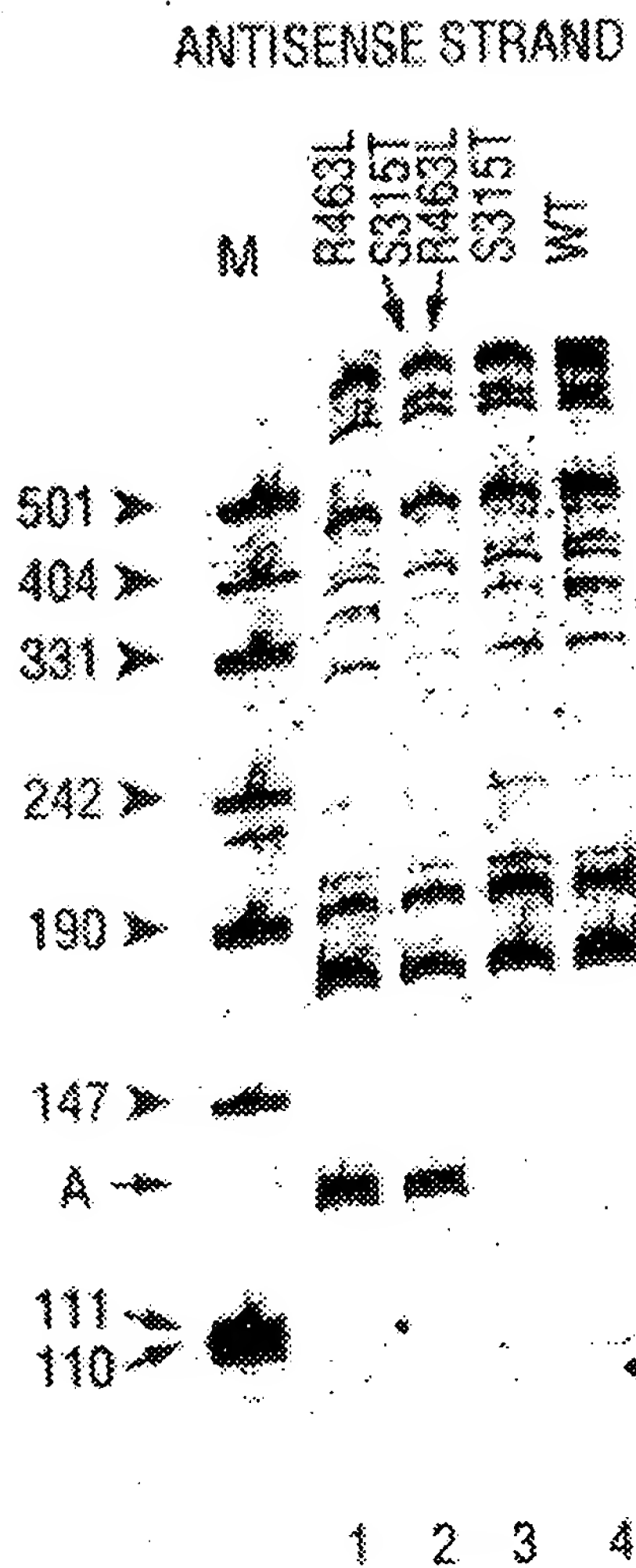


FIG. 87



10	20	30	40	50	60
AGA GTTTGATCCT GGCTCAG					
AAATTGAAGA GTTTGATCAT <u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCCAA		
TTTAACTTCT CAAACTAGTA CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT		1638
70	80	90	100	110	120
				GGCGGAC	GGGTGAGTAA
GTCGAACGGT AACAGGAAGA AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	<u>GGGTGAGTAA</u>		
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACATCATT		ER10
130	140	150	160	170	180
TGCTCTGGGAA ACTGCCCTGAT GGAGGGGGAT	AACACTGGA	AACGGTAGCT	AATACCGCAT		
ACAGACCCCTT TGACGGACTA CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA		
190	200	210	220	230	240
AACGTCGCAA GACCAAAGAG GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG		
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC		
250	260	270	280	290	300
GGATTAGCTA GTAGGTGGGG TAACGGCTCA	CCTAGGCGAC	GATCCCCTAGC	TGGTCTGAGA		
CCTAATCGAT CATCCACCCC ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT		
310	320	330	340	350	360
GGATGACCAG CCACACTGGA ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG		
CCTACTGGTC GGTGTGACCT TGA	GGATGCCCTC	CGTCGTCACC			1659

FIG. 88A



370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCCG	GTTCGGACTA	CGTCGGTACG	GCGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATTT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATTT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCCG	ATTTCGCGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTTCG	CACCCCTCGT

FIG. 88B



790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCTT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTAAT
TCCAATTTTG	AGTTTACTTA	ACTGCCCCCG	GGCGTGTTCC	CCACCTCGTA	CACCAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCCT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTA
TTACACGGAA	GCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
					SB-1
AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCTTATCC	TTTGTTGCCA	GCGGTCCGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC
GCCCTTGAGT	TTCCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTCAG

FIG. 88C



SB-3
SB-4

1210	1220	1230	1240	1250	1260
ATCATGGCCC	TTA				
ATCATGGCCC	TTACGA				
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG
TAGTACCGGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTCCGCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	CACIIATGCA
				GC	CACTTATGCA
1743					
1390	1400	1410	1420	1430	1440
TCCCCGGGCT	TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT
AGGGCCCCGA	ACATGTGTGG	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA
AGGGCCCCGA	ACATG				
1743					
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAATTGGA	AGCCCTCCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCCA	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCCTTG	GACGCCCAACC	TAGTGGAGGA	AT.....	

FIG. 88D



1638 (SEQ ID NO:151) AGAGTTTGATCCTGGCTCAG
E.colirrsE (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAATACATGCA
Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCA

ER10 (SEQ ID NO:152) GGCGGACGGG
E.colirrsE 60 AGTCGAACGGTAACAG---GAAGAAGCTTGCTTCTTT---GCTGACGAGTGGCGGACGGG
Cam.jejun5 62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGGA-----TTAGTGGCGCACGGG
Stp.aureus 61 AGTCGAGCGAA-----CGGACGAGAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACGGG

ER10 TGAGTAA
E.colirrsE 114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATA
Cam.jejun5 114 TGAGTAAGGTATAGTTAATCTGCCCTACACAGAGGACACAGTTGGAAACGACTGCTAATA
Stp.aureus 113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA

E.colirrsE 175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG
Cam.jejun5 176 CTCTATACTCCTGCTTAACACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
Stp.aureus 175 CCGGATAATATTTTGAACCGCATGGTTCAAAGTGAAAGACGGT-----CTT-----GCTGTCA

E.colirrsE 221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGTAAACGGCTCACCTAGGCGACGA
Cam.jejun5 221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAAATGGCTTACCAAGGCTATGA
Stp.aureus 229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA

E.colirrsE 283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
Cam.jejun5 283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAAGTGGTCCAGACTCCTA
Stp.aureus 291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAAGTGGTCCAGACTCCTA
1659 (COMPL) ACTCCTA

FIG. 89A



E.colirrsE	345	CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCCTGATGCAGCCATGCCCGCGTG
Cam.jejun5	345	CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAACCCCTGACGCAGCAACGCCCGCGTG
Stp.aureus	353	CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCCTGACGGAGCAACGCCCGCGTG
1659 (COMPL)		CGGGAGGCAGCAG
E.colirrsE	407	TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTCGGAGCGTAACCTCCTTTCTTAGGGAAG-----AATT
Stp.aureus	415	AGTGATGAAGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAC
E.colirrsE	468	ACCTTTGCTCATTGACGTTACCCGCAGAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	455	C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	476	-TGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B



E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGCGGTAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGCGGTAAGGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAACCTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGGTCAATTGGAAACCTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C



E.colirrsE	840	C-CTTGA-GGC'GTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAAGTGTAACCGCTGGGAGTACGGTCGC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAAGCACTCCGCCTGGGAGTACGACCGC
E.colirrsE	900	AAGGTTAAACTCAATGAATTGACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5	876	AAGATTAAACTCAAGGAATAGACGGGGACCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAGGAATTGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
E.colirrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAAAT
Cam.jejun5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTATAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGAAGAACCTTACCAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E.colirrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTGTCAGCTCGTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrsE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D



SB-3 (SEQ ID NO:157)		ATGACGTCAAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTCAAGTCATC
E.colirrsE	1142	GGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E.colirrsE	1204	ATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAGCGACCTC
Cam.jejun5	1183	ATGGCCCTTATGCCAGGGCGACACACGTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAACC
E.colirrsE	1266	GGGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GGGAGGTGGAG-CAAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GGGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E



E.colirrsE	1389	CTTGTAACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAGAAGTAGGCTTAACCT
Cam.jejun5	1368	CTTGTAACACCGCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
Stp.aureus	1399	ATTGTACACACCGCCCGTCACACACCGAGAGTTTGTAAACACCCGGAAGCCGGTGGAGTAACCT
1743(compl)		CTTGATAC
E.colirrsE	1451	TCG-GGAGGGCGCTTACCACCTTTGTGATTGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC--T-AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAAGCCG
E.colirrsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
Cam.jejun5	1485	TAGGAGAACCTGCGGTTGGATCACCTCCT-----
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-

FIG. 89F



1 2 3 4 5 6 7 8

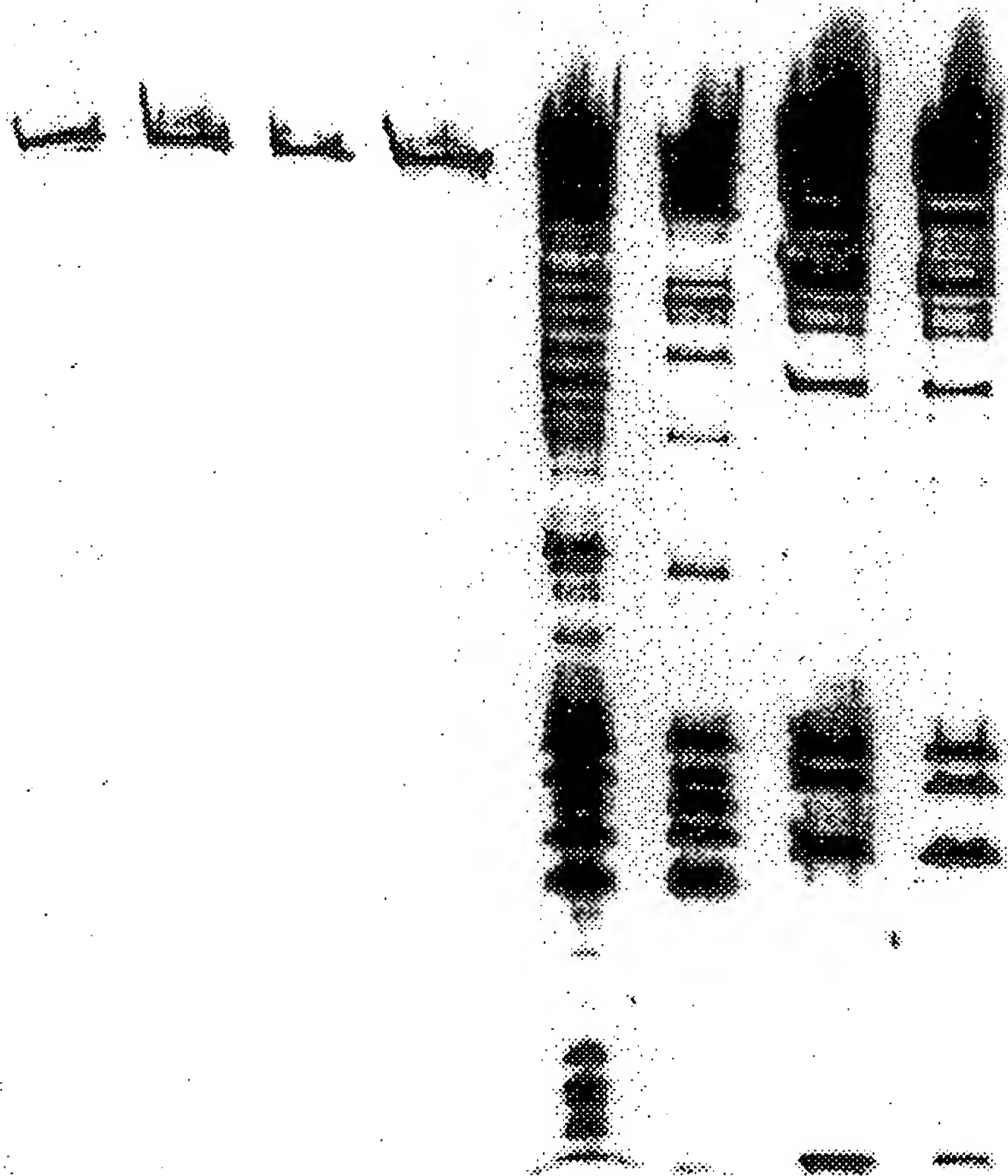


FIG. 90

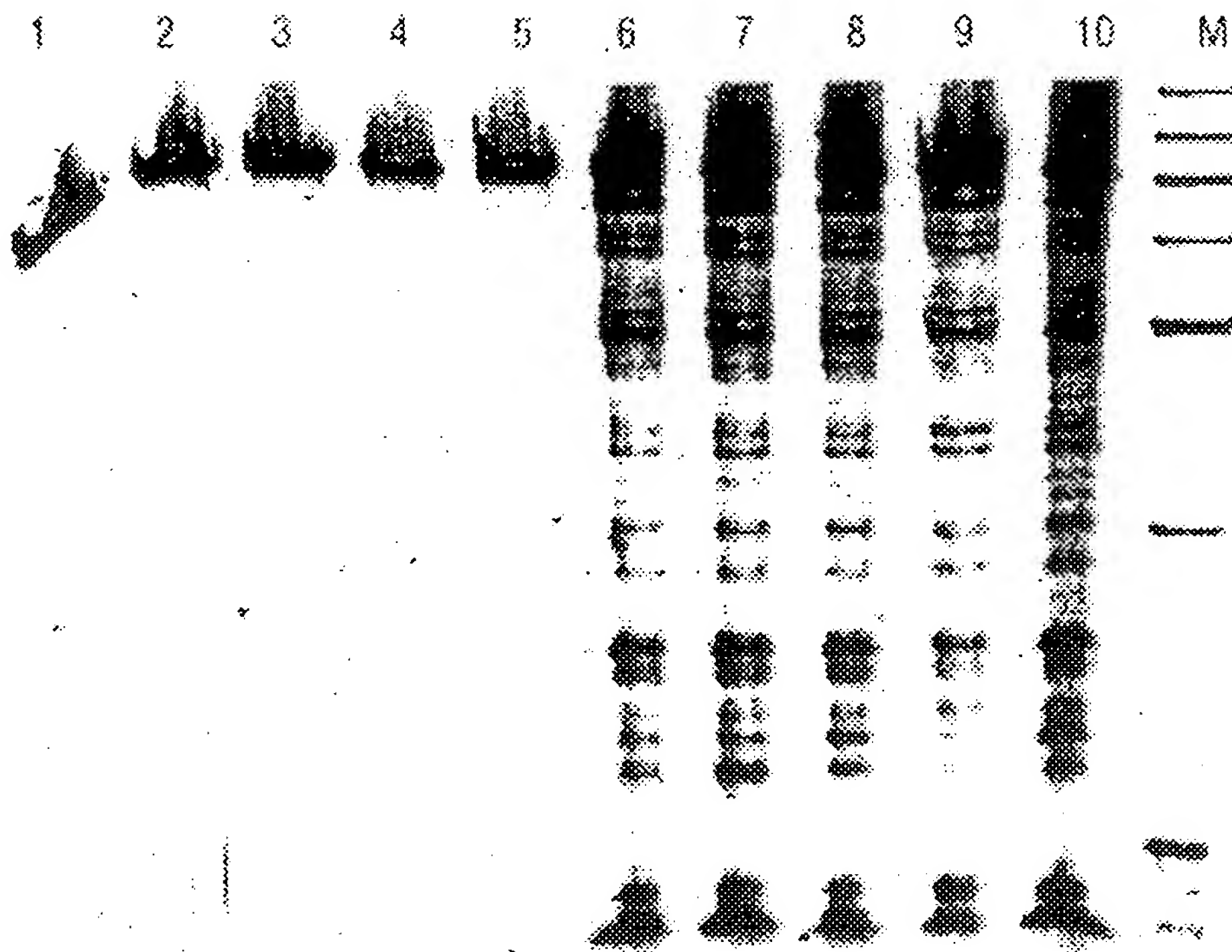


FIG. 91A

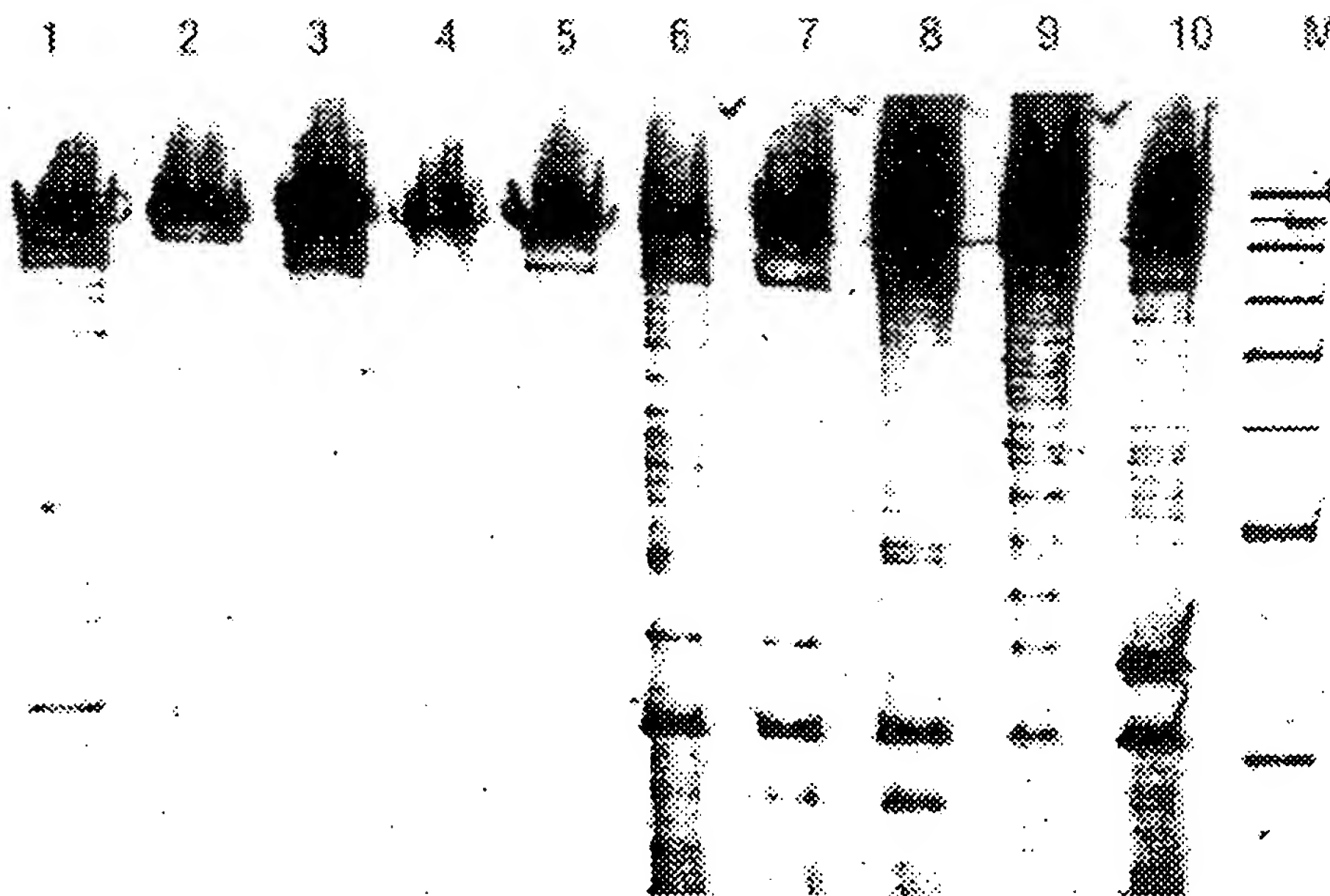


FIG. 91B

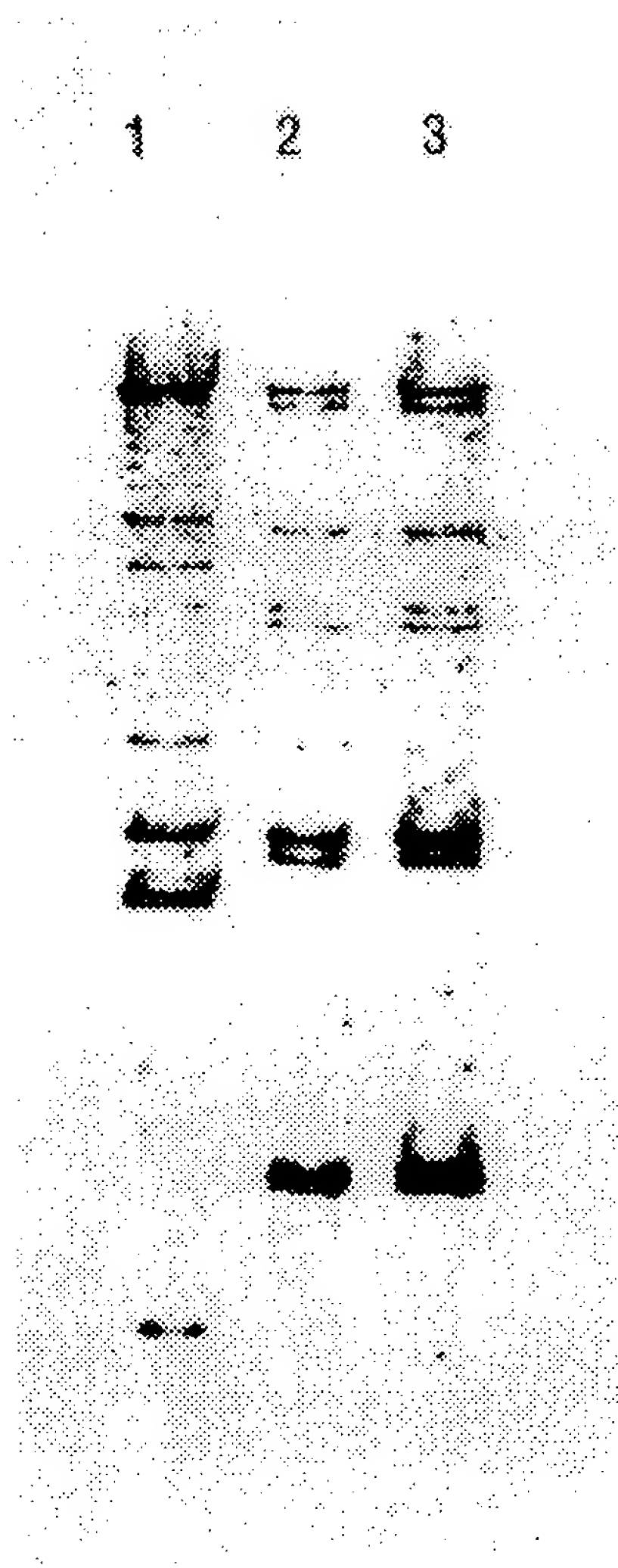


FIG. 92

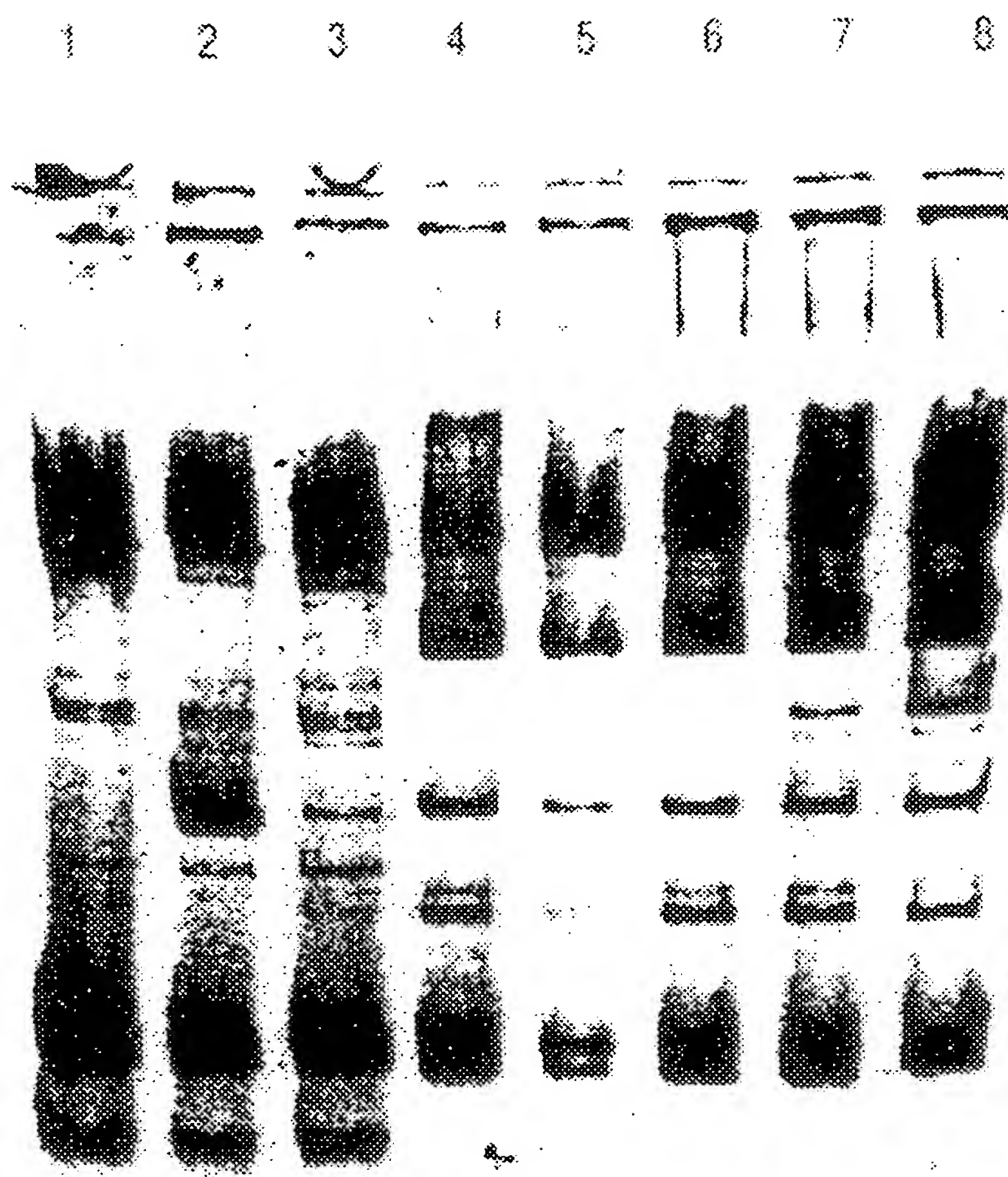


FIG. 93

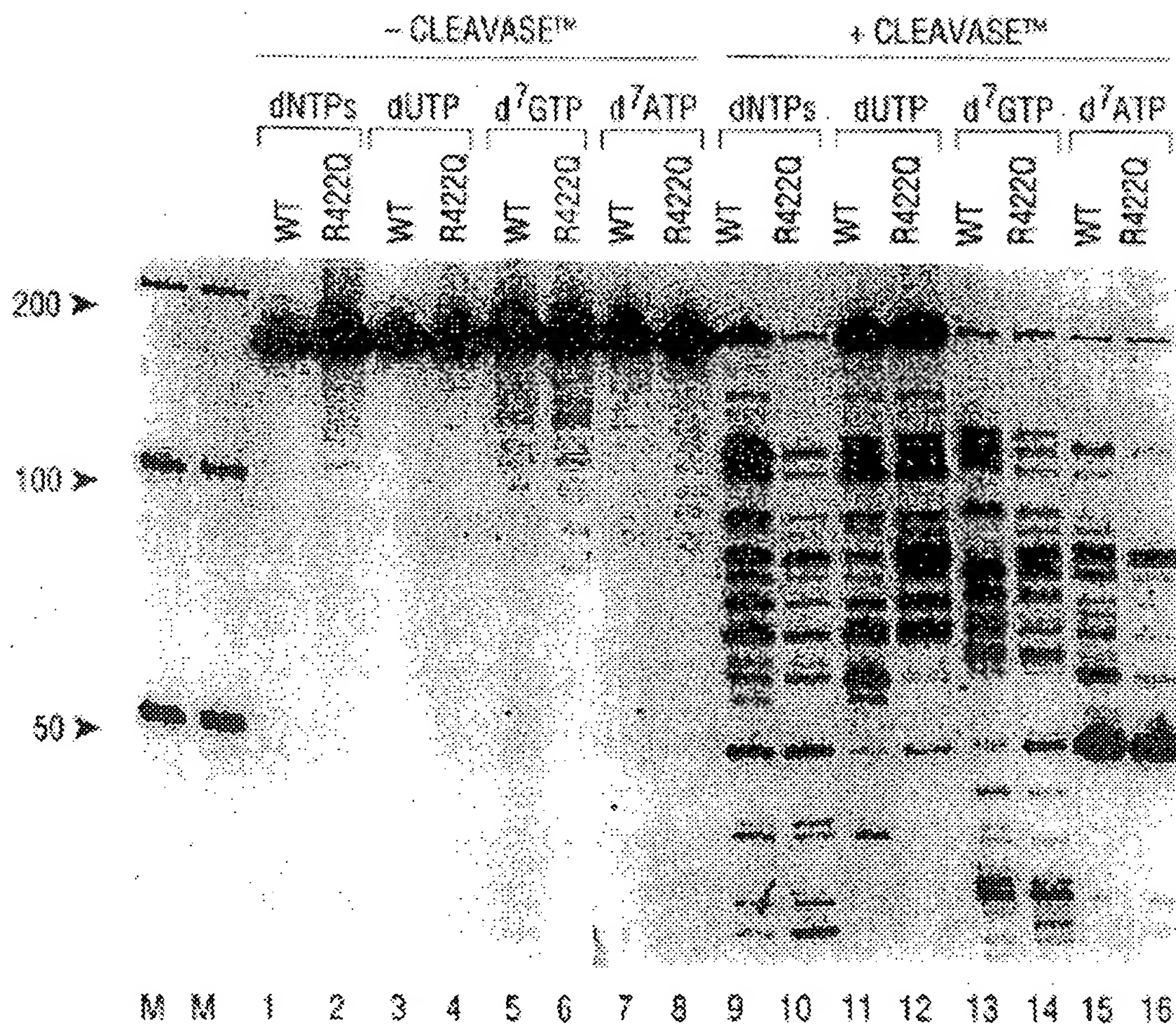


FIG. 94